

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 10:37:22 ; Search time 405 Seconds

(without alignments)
13023.431 Million cell updates/sec

Title: US-09-786-867C-1

Perfect score: 891

Sequence: 1 ttgacaccagacacactggt.....acgacacacataaaaaaa 891

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*

- 1: Geneseqn1980a:*
- 2: Geneseqn1990a:*
- 3: Geneseqn1990b:*
- 4: Geneseqn2000a:*
- 5: Geneseqn2001a:*
- 6: Geneseqn2001b:*
- 7: Geneseqn2002a:*
- 8: Geneseqn2002b:*
- 9: Geneseqn2003a:*
- 10: Geneseqn2003b:*
- 11: Geneseqn2003cs:*
- 12: Geneseqn2004a:*
- 13: Geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	3	AAA13648
2	864.8	97.1	891	3	AAA13614
3	861.6	96.7	891	3	AAA13615
4	852	95.6	868	3	AAA13647
5	373.8	42.0	567	6	ABK55135
6	373.8	42.0	583	9	ACH40379
7	373.8	42.0	630	12	ADQ84434
8	373.8	42.0	630	12	ADQ82261
9	373.8	42.0	630	13	ADQ85218
10	373.8	42.0	630	13	ACN39230
11	373.8	42.0	790	4	AAH02927
12	373.8	42.0	801	12	ADQ29634
13	373.8	42.0	801	13	ADP24690
14	373.8	42.0	830	11	ACN88431
15	373.8	42.0	920	4	AAH23073
16	373.8	42.0	998	8	ACA03888
17	373.8	42.0	1078	6	ABN59686
18	373.8	42.0	1326	8	ACA03889
19	373.8	42.0	2311	8	ACC46705
20	373.4	41.9	791	6	ABK55442

21	373	41.9	1119	8	ABZ71972	Abz71972 Human fer
22	373	41.9	1198	6	ABK83853	Abk83853 Human cDN
23	373	41.9	1198	6	ABN95676	Abn95676 Gene #217
24	372.2	41.8	776	6	ABK55419	Abk55419 Human col
25	372.2	41.8	900	6	ABK34273	Abk34273 Human cDN
26	372.2	41.8	938	10	ADD22487	Add22487 HLA-B46 T
27	372.2	41.8	938	10	ADI15962	Adi15962 Human pp
28	371	41.6	593	6	ABK55034	Abk55034 Human col
29	369.4	41.5	456	9	ACH36218	Ach36218 Human end
30	367	41.2	545	6	ABK55117	Abk55117 Human col
31	367	41.2	550	6	ABK55144	Abk55144 Human col
32	361.8	40.6	654	4	AAK56386	Aak56386 Human cDN
33	361.8	40.6	2311	8	ACC46705	Acc46705 Human dit
34	361.4	40.6	566	9	ACH40217	Ach40217 Human foe
35	357.8	40.2	574	9	ACH42084	Ach42084 Human foe
36	356.6	40.0	489	9	ACH32572	Ach32572 Human end
37	353	39.6	847	13	ACN39288	Acn39288 Tumour-as
38	351.8	39.5	494	12	ADO41255	Ado41255 Human cDN
39	351.8	39.5	549	2	AAQ85979	Aaq85979 Human mon
40	351.8	39.5	570	9	ACH40358	Ach40358 Human foe
41	351.8	39.5	626	13	ACN38870	Acn38870 Tumour-as
42	351.8	39.5	1053	6	AAK594801	Aak594801 Human DNA
43	351.8	39.5	1089	12	ADQ82747	Adq82747 Recombina
44	350.6	39.3	736	13	ACN38201	Acn38201 Tumour-as
45	350.2	39.3	552	11	ADN31064	Adn31064 Human H-C

ALIGNMENTS

RESULT 1

AAA13648

ID AAA13648 standard; cDNA; 891 BP.

XX AAA13648;

DT 20-JUL-2000 (first entry)

XX Human oncofoetal ferritin 1 clone T16 nucleotide sequence in Figure 7.

XX Human; oncofoetal ferritin 1; OFF1; ferritin; transplantaion;

KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;

KW contraceptive; abortive; nontropic; vaccine; immunisation; cancer;

KW transplant rejection; autoimmune disease; fertilisation; diagnosis;

KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;

KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;

KW spontaneous abortion; miscarriage; premature contraction; toxemia;

KW premature delivery; ss.

XX Homo sapiens.

XX WO200015788-A2.

XX 23-MAR-2000.

XX 08-SEP-1999; 99WO-IL0000485.

XX 11-SEP-1998; 98IL-00126181.

XX (GARD-) GARDINO INVESTMENT NV.

XX Moroz C;

XX WPI; 2000-271427/23.

XX DNA sequence coding for oncofetal ferritin 1 protein, useful for

immunitations against breast cancer, for enhancing fertilization rates

during in vitro fertilization treatment and for use as a growth factor of

bone-marrow progenitor cells.

XX Example 7; Fig 7; 66pp; English.

XX The present sequence represents a cDNA clone designated T16 for coding

oncofetal ferritin 1 (OFF1) protein. OFF1 has cytostatic, immunosuppressive, contraceptive, abortive and neutropic activities, and can be used as a vaccine. Compositions comprising the expression vector containing an OFF1 coding sequence, and the OFF1 protein, are useful: (a) for immunisations against cancer, especially breast cancer; (b) in the treatment of transplant rejection, autoimmune diseases, pathological pregnancies; (c) for enhancing fertilisation rates during in vitro fertilisation (IVF) treatment; and (d) for use as a growth factor of bone marrow progenitor cells such as granulocyte monocytes. The OFF1 nucleotide sequence is useful for diagnosing cancer such as breast cancer, hepatoblastoma, leukaemia, Hodgkin's and non-Hodgkin's lymphomas and embryonal tumours, Down's Syndrome, and pathological pregnancies such as spontaneous abortion and miscarriage, premature contractions, toxemia or premature delivery

Sequence 891 BP; 246 A; 268 C; 158 G; 219 T; 0 U; 0 Other;

Query Match 100.0%; Score 891; DB 3; Length 891;
Best Local Similarity 100.0%; Pred. No. 6.6e-260;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGACACAGACCAACTGGTAATGTAGCGCGGCTGAGCTGGGAATTCCTCAAAATG 60
1 TTGACACAGACCAACTGGTAATGTAGCGCGGCTGAGCTGGGAATTCCTCAAAATG 60
61 TAATGCACACTCCATTGCATTCAGCGCGCTCTCTTAGTCGCGCCATGACGACCGGT 120
61 TAATGCACACTCCATTGCATTCAGCGCGCTCTCTTAGTCGCGCCATGACGACCGGT 120
121 CCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCGCAGA 180
121 CCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCGCAGA 180
181 TCAACTGGAGCTCTACGCTCTCTACGTTTACCTGTCTTACTCTTACTCTTACCGCG 240
181 TCAACTGGAGCTCTACGCTCTCTACGTTTACCTGTCTTACTCTTACTCTTACCGCG 240
241 ATGATGTGCTTTGAAGAACTTTGCAAAATCTTCTTCAACATCTCATGAGGAGGG 300
241 ATGATGTGCTTTGAAGAACTTTGCAAAATCTTCTTCAACATCTCATGAGGAGGG 300
301 AACATGCTGAGAACTGATGAAGTGTGAGAACCAACAGAGGTGGCGAATCTCTCTCAGG 360
301 AACATGCTGAGAACTGATGAAGTGTGAGAACCAACAGAGGTGGCGAATCTCTCTCAGG 360
361 ATATCAAGAAACACGACTGTGATGCTGGAGAGCGGCTGAATGCAATGAGTGTGCAT 420
361 ATATCAAGAAACACGACTGTGATGCTGGAGAGCGGCTGAATGCAATGAGTGTGCAT 420
421 TACATTTGGAAAAAATGTGAATCAGTCACTACTGGAATTCCTTCTCTATCTCTCCA 480
421 TACATTTGGAAAAAATGTGAATCAGTCACTACTGGAATTCCTTCTCTATCTCTCCA 480
481 GTCTAGCTGTGGCATCTACTACTACTAAGACCGGCACTCAACACCACTTCTTC 540
481 GTCTAGCTGTGGCATCTACTACTACTAAGACCGGCACTCAACACCACTTCTTC 540
541 GACCCGCGGAGGAGAGACCCCACTTATACCAACCACTTCTGATTTTTCGGTCAC 600
541 GACCCGCGGAGGAGAGACCCCACTTATACCAACCACTTCTGATTTTTCGGTCAC 600
601 CTGAAGTTTATATTCTTATCTTACAGGCTTGGAAATATCTCCATTTGTAACTTAC 660
601 CTGAAGTTTATATTCTTATCTTACAGGCTTGGAAATATCTCCATTTGTAACTTAC 660
661 TACTCCGGAATCGCTGTGCTTACCGCTTACATTTACTGCGAGGCACTTCTATGAC 720
661 TACTCCGGAATCGCTGTGCTTACCGCTTACATTTACTGCGAGGCACTTCTATGAC 720
721 CTAATTGGAAGGCCACCTAGCAATATCAACCACTTAACTTCCCTTACACTTATCATC 780
721 CTAATTGGAAGGCCACCTAGCAATATCAACCACTTAACTTCCCTTACACTTATCATC 780

781 TTCAAAATCTTAATTTACTGACTTCTAGAAATCGTGTGCTTAATCAAGCCTAC 840
781 TTCAAAATCTTAATTTACTGACTTCTAGAAATCGTGTGCTTAATCAAGCCTAC 840
841 GTTTTCACACTTCTAGTAAGCCTCTACCTGCGAGCAACACATATAAAAAA 891
841 GTTTTCACACTTCTAGTAAGCCTCTACCTGCGAGCAACACATATAAAAAA 891

RESULT 2

AAAL3614

ID AAAL3614 standard; cDNA; 891 BP.

XX

AC AAAL3614;

XX

DT 20-JUL-2000 (first entry)

XX

DE Human oncofetal ferritin 1 clone T16 nucleotide sequence in Figure 1.

XX

KW Human; oncofetal ferritin 1; OFF1; ferritin; transplantation;

KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;

KW contraceptive; abortive; neutropic; vaccine; immunisation; cancer;

KW transplant rejection; autoimmune disease; fertilisation; diagnosis;

KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;

KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;

KW spontaneous abortion; miscarriage; premature contraction; toxemia;

KW premature delivery; ss.

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OS Homo sapiens.

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OS WO200015788-A2.

PN

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PD 23-MAR-2000.

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XX	PS	Claim 1; SEQ ID NO 27591; 44pp; English.	PD	XX	22-JUL-2004.
XX	CC	The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030073623	XX	PF	15-OCT-2003; 2003WO-US029126.
XX	CC	Sequence 583 BP; 133 A; 193 C; 143 G; 111 T; 0 U; 3 Other;	XX	PR	19-OCT-2002; 2002US-0418988P.
XX	CC	Query Match 42.0%; Score 373.8; DB 9; Length 583;	XX	PA	(GETH) GENENTECH INC.
XX	CC	Best Local Similarity 99.2%; Pred. No. 9.4e-103;	XX	PA	(WUTD/) WU T D.
XX	CC	Mismatches 375; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	XX	PA	(ZHOU/) ZHOU Y.
QY	QY	86 CGCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAGAACTA 145	XX	PI	Wu TD, Zhou Y;
DB	DB	205 CGCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAGAACTA 264	XX	DR	WPI; 2004-534300/51.
QY	QY	146 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 205	XX	PT	New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
DB	DB	265 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 324	XX	PS	Claim 1; SEQ ID NO 1248; 5504pp; English.
QY	QY	206 GTTTTACCTGTCATGTCTTACTTACTTGTGACCGCGATGATGGCTTTGAAGAACTTGC 265	XX	CC	The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
DB	DB	325 GTTTTACCTGTCATGTCTTACTTACTTGTGACCGCGATGATGGCTTTGAAGAACTTGC 384	XX	QY	Sequence 630 BP; 161 A; 180 C; 162 G; 127 T; 0 U; 0 Other;
QY	QY	266 CAAATCTTCTTCCACCACTCATGAGGAGGGAACATCTGAGAACTGTGAAGCT 325	XX	DB	Query Match 42.0%; Score 373.8; DB 12; Length 630;
DB	DB	385 CAAATCTTCTTCCACCACTCATGAGGAGGGAACATCTGAGAACTGTGAAGCT 444	XX	XX	Best Local Similarity 99.5%; Pred. No. 9.8e-103;
QY	QY	326 CGAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAACAGACTGTGATGA 385	XX	XX	Mismatches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB	DB	445 CGAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAACAGACTGTGATGA 504	QY	QY	86 CGCGCTCTCTTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
QY	QY	386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATATTTGGAAAAAATGTGAATCA 445	DB	DB	40 CGCGCTCTCTTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 99
DB	DB	505 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATATTTGGAAAAAATGTGAATCA 564	QY	QY	146 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 205
QY	QY	446 GTCACTACTGGAATTTCC 463	DB	DB	100 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 159
DB	DB	565 GTCACTACTGGAATTTGCC 582	QY	QY	206 GCTTACTCTGTCATGTCTTACTTGTGACCGCGATGATGGCTTTGAAGAACTTGC 265
RESULT 7					
ADQ84434					
ID	ADQ84434	standard; cDNA; 630 BP.			
XX	AC	ADQ84434;			
XX	DT	07-OCT-2004 (first entry)			
XX	XX	Human tumour-associated antigenic target (TAT) cDNA sequence #1248.			
XX	DE	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;			
XX	KW	cancer; cell proliferative disorder; gene; ss.			
XX	OS	Homo sapiens.			
XX	XX	WO2004060270-A2.			
XX	PN				
XX	XX				

160	CGTTTACTGTCCATGTCTTACTACTTGTGACCGGATGATGTGGCTTTGAGAACTTTGC	219
Db		
266	CAATATCTTTCTTCA CCAATCTCATAGAGGAGGGAA CATGCTTGAGAAATCATGTAAGCT	325
Qy		
220	CAATATCTTTCTTCA CCAATCTCATAGAGGAGGGAA CATGCTTGAGAAATCATGTAAGCT	279
Db		
326	GCAGAAACCAACGAGGTGGCCGAATCTTCTTTCAGGATATCAAGAAACCCAGACTGTGATCA	385
Qy		
280	GCAGAAACCAACGAGGTGGCCGAATCTTCTTTCAGGATATCAAGAAACCCAGACTGTGATCA	339
Db		
386	CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTATCTCGAAAAAAATGTGNAATCA	445
Qy		
340	CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTATCTCGAAAAAAATGTGNAATCA	399
Db		
446	GTCACTACTGGAATTCC	462
Qy		
400	GTCACTACTGGAATGC	416
Db		

RESULT 8

ADQ83261
ID ADQ83261 standard; cDNA: 630 BP.

DT 07-OCT-2004 (first entry)

Human tumour-associated antigenic target (TAT) cDNA sequence #75.

KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.

OS Homo sapiens.

XX PN WO2004060270-A2.

22-JUL-2004.

15-OCT-2003; 2003WO-US029126.

18-OCT-2002: 2002US-0418988P.

XX (GETH) GENENTECH INC.

PA (WUTD/} WU T D.

PA (ZHOU/) ZHOU Y.

Wu TD, Zhou Y:

WPI: 2004-534300/51.

New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

PS Claim 1: SEO ID NO 75: 5504pp: English.

The present invention describes an isolated tumour-associated antigenic target (TAR) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) - (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAR) binding organic molecule that binds to the above polypeptide; (10) a

composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 630 BP: 161 A; 180 C; 162 G; 127 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 12; Length 630;

Best Local Similarity 99.5%; Pred. No. 9.8e-103;

Matches	375;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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Qy 86 CCGCCTCTCCTTAGTCGCGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145

RESULT 9

ADQ85218

ID ADQ85218 standard; cDNA; 630 BP.

AC ADQ85218;

07-OCT-2004 (first entry)

Human tumour-associated antigenic target (TAT) cDNA sequence #2032.

human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.

XX
OS
Homo sapiens.

XX PN WO2004060270-A2.

XX	22-JUL-2004.	QY	206	CGTTTACCTGTCATGCTTACTTCTTGTACCGCGATGATGTGGCTTTGAAGAACTTTGC	265
XX	15-OCT-2003; 2003WO-US029126.	Db	160	CGTTTACCTGTCATGCTTACTTCTTGTACCGCGATGATGTGGCTTTGAAGAACTTTGC	219
XX	18-OCT-2002; 2002US-0418988P.	QY	266	CAATATCTTCTTCCAACTCTCATGAGGAGGAGGACATGCTGAGAACTGATGAAGCT	325
XX	(GETH) GENENTECH INC.	Db	220	CAATATCTTCTTCCAACTCTCATGAGGAGGAGGACATGCTGAGAACTGATGAAGCT	279
PA	(WUTD/) WU T D.	QY	326	GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA	385
PA	(ZHOU/) ZHOU Y.	Db	280	GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA	339
PI	Wu TD, Zhou Y;	QY	386	CTGGGAGAGCGGCTGAATGCAATGAGTGTGCAATTCATTTGGAAAAAATGGAATCA	445
XX	WPI; 2004-534300/51.	Db	340	CTGGGAGAGCGGCTGAATGCAATGAGTGTGCAATTCATTTGGAAAAAATGGAATCA	399
XX	New nucleic acid molecule and encoded polypeptide, for diagnosing,	QY	446	GTCACTACTGCAATTC 462	
PT	preventing or treating cell proliferative disorders such as cancer.	Db	400	GTCACTACTGCAATTC 416	
XX	Claim 1; SEQ ID NO 2032; 5504pp; English.				
XX	The present invention describes an isolated tumour-associated antigenic				
CC	target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide				
CC	sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of				
CC	(a); (c) the complement of (a) or (b); (d) a sequence that has 80%				
CC	sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-				
CC	(c). Also described: (1) an expression vector comprising the above				
CC	nucleic acid; (2) a host cell comprising the above expression vector; (3)				
CC	a process for producing a polypeptide; (4) an isolated polypeptide				
CC	comprising: (a) an amino acid sequence encoded by any of the above				
CC	nucleotide sequences; (b) an amino acid sequence encoded by the full-				
CC	length coding region of the above nucleotide sequences; or (c) a sequence				
CC	having at least 80% identical to (a) or (b); (5) a chimeric polypeptide				
CC	comprising the above polypeptide fused to a heterologous polypeptide; (6)				
CC	an isolated antibody that binds to the above polypeptide; (7) a process				
CC	for producing the antibody; (8) an isolated oligopeptide that binds to				
CC	the above polypeptide; (9) a tumour-associated antigenic target (TAT)				
CC	binding organic molecule that binds to the above polypeptide; (10) a				
CC	composition of matter comprising the above (chimeric) polypeptide,				
CC	antibody, oligopeptide or TAT binding organic molecule, in combination				
CC	with a carrier; (11) an article of manufacture comprising a container and				
CC	the composition of matter contained within the container; (12) methods of				
CC	inhibiting the growth of a cell that expresses the above protein, where				
CC	the growth of the cell is at least in part dependent upon a growth				
CC	potentiating effect of the above protein; (13) a method of				
CC	therapeutically treating a mammal having a cancerous tumour comprising				
CC	cells that express the above protein; (14) a method of determining the				
CC	presence of a protein in a sample suspected of containing the protein				
CC	described above; (15) methods of diagnosing the presence of a tumour in a				
CC	mammal; (16) a method for treating or preventing a cell proliferative				
CC	disorder associated with increased expression or activity of the above				
CC	protein; and (17) a method of binding an antibody, oligopeptide or				
CC	organic molecule to a cell that expresses the protein described above.				
CC	The TAT sequences have cytostatic activities, and can be used in gene				
CC	therapy. The composition and methods are useful for diagnosing,				
CC	preventing or treating cancer. The composition is also used for preparing				
CC	a medicament for the therapeutic treatment or diagnostic detection of a				
CC	cell proliferative disorder or cancer. The present sequence represents a				
CC	human TAT cDNA sequence from the present invention.				
XX	Sequence 630 BP; 161 A; 180 C; 162 G; 127 T; 0 U; 0 Other;				
XX	Query Match 42.0%; Score 373.8; DB 13; Length 630;				
XX	Best Local Similarity 99.5%; Pred. No. 9.8e-103;				
XX	Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	86 CGGCTCTCTTAGTCGGCGGCATACGACCGGCTGCACCTTCGAGGTGGCCAGAACTA	145			
Db	40 CGGCTCTCTTAGTCGGCGGCATACGACCGGCTGCACCTTCGAGGTGGCCAGAACTA	99			
QY	146 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTAGCCTCTTA	205			
Db	100 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTAGCCTCTTA	159			
QY	206 CGTTTACCTGTCATGCTTACTTCTTGTACCGCGATGATGTGGCTTTGAAGAACTTTGC	265			
Db	160 CGTTTACCTGTCATGCTTACTTCTTGTACCGCGATGATGTGGCTTTGAAGAACTTTGC	219			
QY	266 CAATATCTTCTTCCAACTCTCATGAGGAGGAGGACATGCTGAGAACTGATGAAGCT	325			
Db	220 CAATATCTTCTTCCAACTCTCATGAGGAGGAGGACATGCTGAGAACTGATGAAGCT	279			
QY	326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA	385			
Db	280 GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA	339			
QY	386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCAATTCATTTGGAAAAAATGGAATCA	445			
Db	340 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCAATTCATTTGGAAAAAATGGAATCA	399			
QY	446 GTCACTACTGCAATTC 462				
Db	400 GTCACTACTGCAATTC 416				
RESULT 10					
ACN39230					
ID	ACN39230 standard; cDNA; 630 BP.				
XX	ACN39230;				
AC					
XX	18-NOV-2004 (first entry)				
DT					
XX	Tumour-associated antigenic target (TAT) cDNA DNA325475, SEQ ID NO:3247.				
DE					
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;				
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;				
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;				
KW	central nervous system cancer; bladder cancer; pancreatic cancer;				
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;				
KW	chromosome identification; chromosome mapping; gene mapping;				
KW	gene therapy; cytostatic; gene; ss.				
OS	Homo sapiens.				
XX					
PN	WO2004030615-A2.				
XX					
PD	15-APR-2004.				
XX					
PF	29-SEP-2003; 2003WO-US028547.				
XX					
PR	02-OCT-2002; 2002US-0414971P.				
XX					
PA	(GETH) GENENTECH INC.				
XX					
PI	Wu TD, Zhang Z, Zhou Y;				
XX					
DR	WPI; 2004-347921/32.				
XX					
PT	New tumor-associated antigenic target polypeptides and nucleic acids,				
PT	useful in preparing a medicament for treating or detecting a				
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or				
PT	prostate cancer or tumor.				
XX					
PS	Claim 1; SEQ ID NO 3247; 7273pp; English.				
XX					
CC	The invention relates to human tumour-associated antigenic target (TAT)				
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are				
CC	overexpressed in cancer tissues compared to normal tissues, and may thus				
CC	serve as effective targets for the diagnosis and treatment of cancer in				
CC	mammals. The invention also relates to the TAT nucleic acids and				
CC	sequences at least 80% identical to the TAT nucleic acids and				
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic				
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic				
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a				
CC	TAT polypeptide; and methods and compositions for the treatment or				
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,				

PR 31-JUL-2003; 2003US-0491397P.
XX (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ;
PI Dwivedi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ, Myerow SH;
PI Brown-Shimer SLA, Thiagalingam A, Thibodeau SN, Molino GA;
XX
XX WPI; 2004-545561/53.
DR P-PSDB; ADQ29701.
XX
XX Diagnosing colon cancer in individual, preferably human, by detecting
PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is
PT indicative of colon cancer in individual.
XX
XX Claim 7; SEQ ID NO 60; 433pp; English.
XX
XX The invention comprises a method for diagnosing colon cancer in an
CC individual, the method involves obtaining a serum sample from the
CC individual and detecting the presence of either TIMP1 or Regl-alpha
CC an additional colorectal cancer-associated marker. The method of the
CC invention is useful for diagnosing colon cancer in an individual. The
CC present DNA sequence represents a human colorectal cancer-associated
CC protein coding sequence of the invention.
XX
SQ Sequence 801 BP; 209 A; 226 C; 187 G; 179 T; 0 U; 0 Other;
Query Match 42.0%; Score 373.8; DB 12; Length 801;
Best Local Similarity 99.5%; Pred. No. 1.1e-102;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 86 CGGCTCTCTTGTAGTGGCGGCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
DB 70 CGGCTCTCTTGTAGTGGCGGCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 129
QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 205
DB 130 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 189
QY 206 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAGAACTTTGTC 265
DB 190 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAGAACTTTGTC 249
QY 266 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAGAGCT 325
DB 250 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAGAGCT 309
QY 326 CGAGAACCAACGAGTGGCCGAATCTTCTTCAAGATATCAAGAAACAGACTGTGATGA 385
DB 310 GCAGAACCAACGAGTGGCCGAATCTTCTTCAAGATATCAAGAAACAGACTGTGATGA 369
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGGCATTACATTTGGAAAAATGTGAATCA 445
DB 370 CTGGGAGAGCGGCTGAATGCAATGGAGTGGCATTACATTTGGAAAAATGTGAATCA 429
QY 446 GTCATCTAGGAATTC 462
DB 430 GTCATCTAGGAATTC 446
RESULT 13
ADP24690
ID ADP24690 standard; cDNA; 801 BP.
XX
XX AC ADP24690;
XX
DT 18-NOV-2004 (first entry)
XX
XX PRO polypeptide encoding cDNA SEQ ID NO:1868.
XX
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;

KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX
OS Unidentified.
XX
FN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-419628/39.
DR P-PSDB; ADP24691.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 1; SEQ ID NO 1868; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatologic, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
SQ Sequence 801 BP; 209 A; 226 C; 187 G; 179 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 13; Length 801;
Best Local Similarity 99.5%; Pred. No. 1.1e-102;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 86 CGGCTCTCTTGTAGTGGCGGCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
DB 70 CGGCTCTCTTGTAGTGGCGGCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 129
QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 205
DB 130 CCACGAGACTCAGAGGCGGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA 189
QY 206 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAGAACTTTGTC 265
DB 190 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAGAACTTTGTC 249

QY 266 CAATATCTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
| | | | |
Db 250 CAATATCTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 309
| | | | |
QY 326 CGAGAACCAACGAGGTGGCCGAATCTTCTTACGAGATATCAAGAAACAGAGCTGTGATGA 385
| | | | |
Db 310 CGAGAACCAACGAGGTGGCCGAATCTTCTTACGAGATATCAAGAAACAGAGCTGTGATGA 369
| | | | |
QY 386 CTGGGAGAGCGGGCTGAATGCAATGAGAGTGTGATTAATTTGGAAAAAATGTGAATCA 445
| | | | |
Db 370 CTGGGAGAGCGGGCTGAATGCAATGAGAGTGTGATTAATTTGGAAAAAATGTGAATCA 429
| | | | |
QY 446 GTCACACTGGAATTC 462
| | | | |
Db 430 GTCACACTGGAATTC 446
| | | | |

RESULT 14

ACN88431

ID ACN88431 standard; DNA; 830 BP.

XX AC

ACN88431;

DT 02-DEC-2004 (first entry)

XX Breast cancer related marker, seq id 9581.

DE Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX Homo sapiens.

XX US2003099974-A1.

XX 29-MAY-2003.

XX 18-JUL-2002; 2002US-00198846.

XX 18-JUL-2001; 2001US-0306220P.

XX (MILL-) MILLENNIUM PHARM INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX WPI; 2003-787014/74.

XX Novel isolated polypeptide associated with breast cancer, useful for
PT detecting presence of polypeptide in sample, as a marker for breast
PT cancer.

XX Disclosure; SEQ ID NO 9581; 36pp; English.

XX The invention relates to an isolated polypeptide (I) associated with
CC breast cancer which is encoded by a nucleic acid molecule comprising a
CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC the polypeptide of the invention. The activity of the polypeptide of the
CC invention may be described as cytostatic. The antibody is useful for
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC invention are useful in the detection of breast tumours. (I) is useful as
CC a marker for breast cancer and in breast cancer therapy. Sequences given
CC in records ACN78851-ACN92934 represent nucleic acid markers associated
CC with breast cancer. Note: The sequence listing does not form part of the
CC specification but may be obtained in electronic format from the USPTO web
CC site at seqdata.uspto.gov/sequence.html?docID=20030099974

XX Sequence 830 BP; 209 A; 224 C; 210 G; 184 T; 0 U; 3 Other;

Query Match 42.0%; Score 373.8; DB 11; Length 830;

Best Local Similarity 99.5%; Pred. No. 1.1e-102;

Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTACTGCGCGCCATGACGACCGGTCACCTCGCAGGTGCGCAGAACTA 145
| | | | |

Db 56 CCGCTCTCTTACTGCGCGCCATGACGACCGGTCACCTCGCAGGTGCGCAGAACTA 115
| | | | |
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 205
| | | | |
Db 116 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 175
| | | | |
QY 206 CGTTTACTCTGCCATGCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGC 265
| | | | |
Db 176 CGTTTACTCTGCCATGCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGC 235
| | | | |
QY 266 CAAATACTTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
| | | | |
Db 236 CAAATACTTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295
| | | | |
QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTACGAGATATCAAGAAACAGAGCTGTGATGA 385
| | | | |
Db 296 GCAGAACCAACGAGGTGGCCGAATCTTCTTACGAGATATCAAGAAACAGAGCTGTGATGA 355
| | | | |
QY 386 CTGGGAGAGCGGGCTGAATGCAATGAGAGTGTGATTAATTTGGAAAAAATGTGAATCA 445
| | | | |
Db 356 CTGGGAGAGCGGGCTGAATGCAATGAGAGTGTGATTAATTTGGAAAAAATGTGAATCA 415
| | | | |
QY 446 GTCACACTGGAATTC 462
| | | | |
Db 416 GTCACACTGGAATTC 432
| | | | |

RESULT 15

AAH23073

ID AAH23073 standard; DNA; 920 BP.

XX AC

AAH23073;

XX 17-SEP-2001 (first entry)

XX Osteoarthritis tissue-derived nucleic acid sequence #3.

XX Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;
KW wound healing; osteopathic; anti-arthritis; anti-inflammatory; vulneryary;
KW antibacterial; antiallergic; ds.

XX Homo sapiens.

XX WO200153531-A2.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US000016.

XX 18-JAN-2000; 2000US-0176523P.

XX (PHAA) PHARMACIA CORP.

XX Phippard D, Vasanthakamur G, Dotson S, Ma X;

XX WPI; 2001-451914/48.

XX Substantially purified protein, polypeptide or their fragments, used to
PT identify a biologically active compound or composition and treat
PT mammalian osteoarthritis.

XX Claim 1; Page 91-92; 144pp; English.

XX Sequences AAH23071-23152 represent nucleic acid sequences derived from
CC osteoarthritis tissues. The sequences are useful as probes and for the
CC diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides
CC and polypeptides of the invention are useful for generating diagnostic
CC reagents, as targets for small molecule drug development, generation of
CC therapeutics, and cloning genes. Specific antibodies are used to generate
CC enzyme linked immunosorbent assays for detection of osteoarthritis. The
CC invented molecules can be used to treat osteoarthritis or to analyse the
CC disease-modifying activity of osteoarthritis drugs. Other disorders
CC treatable using the nucleic acid sequences include atopic, inflammatory

CC and infectious disorders e.g. Crohn's disease and sepsis, and wound
CC healing

XX

SQ Sequence 920 BP; 233 A; 272 C; 216 G; 199 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 4; Length 920;
Best Local Similarity 99.5%; Pred. No. 1.2e-102;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	86	CGCCCTCTCCTTAGTCGGCGCCATCAGACGCGTCCACCTCGCAGGTGCGCCAGAACTA	145
Db	173	CGCCCTCTCCTTAGTCGGCGCCATCAGACGCGTCCACCTCGCAGGTGCGCCAGAACTA	232
QY	146	CCACCAGGACTCAGAGGCGCCATCAACCGCAGATCAACCTGGAGCTCTAGCCTCCTA	205
Db	233	CCACCAGGACTCAGAGGCGCCATCAACCGCAGATCAACCTGGAGCTCTAGCCTCCTA	292
QY	206	CGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC	265
Db	293	CGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC	352
QY	266	CAATATCTTTCTTACCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT	325
Db	353	CAATATCTTTCTTACCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT	412
QY	326	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA	385
Db	413	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA	472
QY	386	CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTGGAAAAAATGTGAATCA	445
Db	473	CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTGGAAAAAATGTGAATCA	532
QY	446	GTCCTACTCTGGAATTC	462
Db	533	GTCCTACTCTGGAATTC	549

Search completed: April 1, 2005, 11:40:54
Job time : 409 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:28:57 ; Search time 141 Seconds
(without alignments)
10339.876 Million cell updates/sec

Title: US-09-786-867C-1
Perfect score: 891
Sequence: 1 ttgacaccagaccactgggt.....acgacacacataaaaaaa 891

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	373.8	42.0	1462	4	US-09-949-016-4902
2	350	39.3	491	3	US-09-643-597-307
3	350	39.3	491	4	US-09-480-884A-307
4	350	39.3	491	4	US-09-542-615A-307
5	350	39.3	491	4	US-09-606-421B-307
6	350	39.3	491	4	US-09-630-940B-307
7	348.6	39.1	924	4	US-09-919-172-94
8	348.6	39.1	924	4	US-09-976-594-1076
9	341.8	38.4	9364	4	US-09-949-016-14890
10	309.6	34.7	933	4	US-09-799-451-404
11	293	32.9	32065	4	US-09-949-016-12136
12	293	32.9	32066	4	US-09-949-016-13268
13	237.2	26.6	292	4	US-09-313-294A-6635
14	225.4	25.3	601	4	US-09-949-016-115137
15	222	24.9	396	4	US-09-640-173-7
16	222	24.9	396	4	US-09-713-550-7
17	222	24.9	396	4	US-09-825-294-7
18	222	24.9	396	4	US-09-970-966-7
19	215	24.1	506	4	US-09-621-976-542
20	213.2	23.9	440	3	US-09-397-787-328
21	211.4	23.7	396	4	US-09-640-173-64
22	211.4	23.7	396	4	US-09-713-550-64
23	211.4	23.7	396	4	US-09-825-294-64
24	211.4	23.7	396	4	US-09-970-966-64
25	207.4	23.3	1613	1	US-08-219-842-1
26	207.4	23.3	1613	1	US-08-451-096-1
27	207.4	23.3	1613	2	US-08-810-599-1

28	207.4	23.3	1735	3	US-08-413-740A-1	Sequence 1, Appli
29	207.4	23.3	1735	5	PCT-US95-04063-1	Sequence 1, Appli
30	207.4	23.3	16568	4	US-09-525-906-1	Sequence 1, Appli
31	207.4	23.3	16569	3	US-09-097-889-2	Sequence 2, Appli
32	207.4	23.3	16569	3	US-09-377-856-1	Sequence 1, Appli
33	207.4	23.3	16569	3	US-09-302-681-2	Sequence 2, Appli
34	207.4	23.3	16569	4	US-09-098-079-2	Sequence 2, Appli
35	207.4	23.3	16569	4	US-10-053-611-1	Sequence 1, Appli
36	205.8	23.1	1539	4	US-09-377-497-3	Sequence 3, Appli
37	205	23.0	366	4	US-09-401-064-338	Sequence 338, App
38	204.2	22.9	6744	3	US-09-097-889-1	Sequence 1, Appli
39	204.2	22.9	6744	4	US-09-098-079-1	Sequence 1, Appli
40	201	22.6	6691	3	US-09-302-681-3	Sequence 3, Appli
41	200.6	22.5	601	4	US-09-949-016-91636	Sequence 91636, A
42	199.4	22.4	112623	4	US-09-949-016-14374	Sequence 14374, A
43	169.8	19.1	241	4	US-09-389-681-332	Sequence 332, App
44	169.8	19.1	241	4	US-09-620-405B-332	Sequence 332, App
45	169.8	19.1	241	4	US-09-433-826B-332	Sequence 332, App

ALIGNMENTS

RESULT 1

US-09-949-016-4902
; Sequence 4902, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4902
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4902

Query Match	42.0%	Score	373.8;	DB	4;	Length	1462;
Best Local Similarity	99.5%	Pred. No.	1.6e-107;				
Matches	375;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
QY	86	CGCGCTCTCTTAGTTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGGCGAAGCTA	145				
Db	187	CGCGCTCTCTTAGTTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGGCGAAGCTA	246				
QY	146	CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTTA	205				
Db	247	CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTTA	306				
QY	206	CGTTTACCTGTCATGCTTACTACTTACTTACCGCGCATGATGGCTTTGAAGAACTTTGC	265				
Db	307	CGTTTACCTGTCATGCTTACTACTTACTTACCGCGCATGATGGCTTTGAAGAACTTTGC	366				
QY	266	CAATATCTTCTTCCACCAATCTCATGAGGAGGGAACATCTGAGAACTGATCAAGCT	325				
Db	367	CAATATCTTCTTCCACCAATCTCATGAGGAGGGAACATCTGAGAACTGATCAAGCT	426				
QY	326	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAAGATATCAAGAACACAGACTGTGATGA	385				
Db	427	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAAGATATCAAGAACACAGACTGTGATGA	486				
QY	386	CTGGAGAGCGGGCTGGAATGCAATGGAATGATGTCATTACATTGGAAAAAATGTGAATCA	445				

Db 487 GTGGAGAGCGGCTGAATGCAATGAGTGTGCTTACATTGGAAAAAATGTGAATCA 546
Qy 446 GTCACTACTGGAATCC 462
Db 547 GTCACTACTGGAATGC 563

RESULT 2

US-09-643-597-307
; Sequence 307, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-643-597-307

Query Match 39.3%; Score 350; DB 3; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 CCGCTCTCTTCTAGTCCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 145
Db 142 CCGCTCTCTTCTAGTCCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 201
Qy 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
Db 202 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261
Qy 206 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 262 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321
Qy 266 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 322 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 381
Qy 326 GCAGAACCAACGAGGTGCGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 382 GCAGAACCAACGAGGTGCGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 441
Qy 386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCTTACATTGGAAAAA 435
Db 442 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCTTACATTGGAAAAA 491

RESULT 3

US-09-480-884A-307
; Sequence 307, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; CURRENT FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-480-884A-307

Query Match 39.3%; Score 350; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 CCGCTCTCTTCTAGTCCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 145
Db 142 CCGCTCTCTTCTAGTCCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 201
Qy 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
Db 202 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261
Qy 206 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 262 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321
Qy 266 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 322 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 381
Qy 326 GCAGAACCAACGAGGTGCGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 382 GCAGAACCAACGAGGTGCGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 441
Qy 386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCTTACATTGGAAAAA 435
Db 442 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCTTACATTGGAAAAA 491

RESULT 4

US-09-542-615A-307
; Sequence 307, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: 210121.455C8

; CURRENT APPLICATION NUMBER: US/09/542,615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-542-615A-307

Query Match 39.3%; Score 350; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 145
|
Db 142 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 201
|
QY 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
|
Db 202 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261
|
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
|
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321
|
QY 266 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 325
|
Db 322 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 381
|
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
|
Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 441
|
QY 386 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 435
|
Db 442 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 491
|

RESULT 5

US-09-606-421B-307
; Sequence 307, Application US/09606421B
; Patent No. 6531315

GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B

; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-606-421B-307

Query Match 39.3%; Score 350; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 145
|
Db 142 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 201
|
QY 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
|
Db 202 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261
|
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
|
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321
|
QY 266 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 325
|
Db 322 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 381
|
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
|

Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 441
|
QY 386 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 435
|
Db 442 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 491
|

RESULT 6

US-09-630-940B-307
; Sequence 307, Application US/09630940B
; Patent No. 6737514

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C10

; CURRENT APPLICATION NUMBER: US/09/630,940B

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 367

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-630-940B-307

Query Match 39.3%; Score 350; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 145
|
Db 142 CCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 201
|
QY 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
|
Db 202 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261
|
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
|
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321
|
QY 266 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 325
|
Db 322 CAATACCTTTCTTACCACCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 381
|
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
|
Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 441
|
QY 386 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 435
|
Db 442 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAA 491
|

RESULT 7

US-09-919-172-94
; Sequence 94, Application US/09919172
; Patent No. 6673545

GENERAL INFORMATION:

; APPLICANT: Farris, Mary

; APPLICANT: Turner, Christopher M.

;; TITLE OF INVENTION: PROSTATE CANCER MARKERS
;; FILE REFERENCE: PA-0036 US
;; CURRENT APPLICATION NUMBER: US/09/919,172
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/222,469
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PERL Program
;; SEQ ID NO 94
;; LENGTH: 924
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6673545 1382920.38
US-09-919-172-94

Query Match 39.1%; Score 348.6; DB 4; Length 924;
Best Local Similarity 98.4%; Pred. No. 1.1e-99;
Matches 373; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 86 CGCCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCT-CGCAGGTG-CGCCAGAAC 143
DB 184 COTCCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCTCGCGAGGTGCGCCAGAAC 243

QY 144 TACCACAGGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 203
DB 244 TACCACAGGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 303

QY 204 TAGCTTTACCTGTCATGCTTACTTACTTTGACCGCGATGATGTGGCTTTGAAGAATTT 263
DB 304 TAGCTTTACCTGTCATGCTTACTTACTTTGACCGCGATGATGTGGCTTTGAAGAATTT 363

QY 264 GCCAATCTCTTCCACCAATCTCATGAGGAGGGAACATCTCGAGAACTGATGAAG 323
DB 364 GCCAATCTCTTCCACCAATCTCATGAGGAGGGAACATCTCGAGAACTGATGAAG 423

QY 324 CTGCAGAACCAACGAGGTGGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGAT 383
DB 424 CTGCAGAACCAACGAGGTGGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGAT 483

QY 384 GACTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 443
DB 484 GACTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 543

QY 444 CAGTCACTACTGGAATTC 462
DB 544 CAGTCACTACTGGAATTC 562

RESULT 8
US-09-976-594-1076
; Sequence 1076, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1076
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1382920.38
US-09-976-594-1076

Query Match 39.1%; Score 348.6; DB 4; Length 924;
Best Local Similarity 98.4%; Pred. No. 1.1e-99;
Matches 373; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 86 CGCCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCT-CGCAGGTG-CGCCAGAAC 143
DB 184 COTCCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCTCGCGAGGTGCGCCAGAAC 243

QY 144 TACCACAGGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 203
DB 244 TACCACAGGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 303

QY 204 TAGCTTTACCTGTCATGCTTACTTACTTTGACCGCGATGATGTGGCTTTGAAGAATTT 263
DB 304 TAGCTTTACCTGTCATGCTTACTTACTTTGACCGCGATGATGTGGCTTTGAAGAATTT 363

QY 264 GCCAATCTCTTCCACCAATCTCATGAGGAGGGAACATCTCGAGAACTGATGAAG 323
DB 364 GCCAATCTCTTCCACCAATCTCATGAGGAGGGAACATCTCGAGAACTGATGAAG 423

QY 324 CTGCAGAACCAACGAGGTGGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGAT 383
DB 424 CTGCAGAACCAACGAGGTGGCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGAT 483

QY 384 GACTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 443
DB 484 GACTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 543

QY 444 CAGTCACTACTGGAATTC 462
DB 544 CAGTCACTACTGGAATTC 562

RESULT 9
US-09-949-016-14890/C
; Sequence 14890, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14890
; LENGTH: 93364
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(93364)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14890

Query Match 38.4%; Score 341.8; DB 4; Length 93364;
Best Local Similarity 94.2%; Pred. No. 2.7e-96;
Matches 355; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 86 CGCCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCTCGCGAGGTGCGCCAGAATA 145
DB 40904 CCACCTCTCCTTAGTCGCGCCGATGACGACCGCGTCCACCTCGCGAGGTGCGCCAGAATA 40845

QY 146 CCACCGAGCTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTA 205
|||||

Db 40844 CCACCAGGACTCAGAGCGCGCATCAACGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 40785
Qy 206 CGTTTACCTGTCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 40784 CGTTTACCTGTCGCTGCTTACAACTTTGACCGCGATGATGGCTTTGAGGAACCTTTGC 40725
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 40724 CACATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCCGAGAACTGATGAAGCT 40665
Qy 326 GCAGAACCAACGAGGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 40664 GCAGAACTATCGTGGTGGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 40605
Qy 386 CTGGAGAGCGGCTGGAATGCAATGAGTGTGCATTTGGAAGAAAAATGGAATCA 445
Db 40604 CTGGAGAGTGGGCTGGAATGCAATGAGTGTGCATTTGGAAGAAAAATGGAATCA 40545
Qy 446 GTCACCTACTGGAATCC 462
Db 40544 GTCACCTATTTGGAATGCC 40528

RESULT 10

US-09-799-451-404
; Sequence 404, Application US/09799451
; Patent No. 6783969

GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 404
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (155)..(694)

US-09-799-451-404

Query Match 34.7%; Score 309.6; DB 4; Length 933;

Best Local Similarity 90.7%; Pred. No. 2.4e-87;

Matches 330; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 99 GTCGCGGCATGACGACCGCTCCACCTCGAGGTGGCGCAGAACTACACGAGACTCA 158
Db 146 GCCGCCACATGACACCGCGCTCCCTCGGAAGTGGCGCAACTACACGAGACGCG 205
Qy 159 GAGGCGGCATCAACCGCGCAGATCAACCTGGAGCTCTAGCGCTCTTACCTGTCC 218
Db 206 GAGGCTGCATCAACCGCGCAGATCAACCTGGAGTGTATGCTCTCTATCTGTCT 265

Qy 219 ATGCTTACTACTTTGACCGGATGATGCTGCTTTGAAGAACTTTGCCAATACTTTCTT 278
Db 266 ATGCTTGTATTATTTGACCGGATGATGCTGCTTTGAAGAACTTTGCCAATACTTTCTC 325
Qy 279 CACCAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGA 338
Db 326 CACCAATCTCATGAGGAGGGAACATGCCGAGAACTGATGAAGCTGCAGAACCAACGA 385
Qy 339 GGTGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGCTGGGAGAGCGGG 398
Db 386 GGTGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGCTGGGAGAGCGGG 445
Qy 399 CTGAATGCAATGGAGTGTGCATTTGGAAGAAAAATGGAATCAGTCACTACTGNA 458
Db 446 CTGAATGCAATGGAGTGTGCATCTGCACCTTGGAAGAAAGTGTGAATCAGTCACTACTGNA 505
Qy 459 TTCC 462
Db 506 CTGC 509

RESULT 11

US-09-949-016-12136
; Sequence 12136, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12136
; LENGTH: 32065
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(32065)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12136

Query Match 32.9%; Score 293; DB 4; Length 32065;

Best Local Similarity 87.3%; Pred. No. 3.9e-81;

Matches 357; Conservative 0; Mismatches 20; Indels 32; Gaps 2;

Qy 86 CCGCTCTCTCTAGTGGCGGCATGACGACCGGCTCCACCTCGCAGGTGGCGCAGACTA 145
Db 17986 CCGCTCTCTCTAGTGGCGGCATGACGACCGGCTCTACCTCGCAGGTGGCGCAGACTA 18045
Qy 146 CCACGAGACTCAGAGCGCGCATCAACCGCGCAGATCAACCTGGAGCTCTAGCCCTCTTA 205
Db 18046 CCACGAGACTCAGAGCGCGCATCAACCGCGCAGATCAACCTGGAGCTCTAGCCCTCTTC 18105
Qy 206 CGTTTACCTGTCATGCTTACTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 265
Db 18106 CATTTACCTGTCGCTTACTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 18165
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 18166 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 18225
Qy 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATG- 384

Db 18226 GTAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACAGACTGTGCGG 18285
Qy 385 -----ACTGGGAGCGGCTGAATGCAATG-----AG 413
Db 18286 GAGATGCGATGGGAGACGGGCTGAATGCGATGATACATTTGGAAAAAATGTGCGAT 18345
Qy 414 TGTGCATTACATTTGGAAAAAATGTGAATCAGTCAGTCATCTGGAATTC 462
Db 18346 TTTGCATTACATTTGGAAAAAATGTGAATCAGTCAGTCATCTGGAATTC 18394

RESULT 12

US-09-949-016-13268
; Sequence 13268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13268
; LENGTH: 32066
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(32066)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13268

Query Match 32.9%; Score 293; DB 4; Length 32066;

Best Local Similarity 87.3%; Pred. No. 3.9e-81; Mismatches 20; Indels 32; Gaps 2;

Matches 357; Conservative 0;

Qy 86 CGCCTCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
Db 17986 CGCCTCTCTCTTAGTGGCGGCATGACGACCGCGTCTACCTCGCAGGTGCGCCAGAACTA 18045
Qy 146 CCACGAGACTCAGAGCGCGCATCAACGCGCAGATCAACCTGGAGCTCTACGCTCTCTA 205
Db 18046 CCACCAAGACTCAGAGCGCGCATCAACGCGCAGATCAACCTGGAGCTCTACGCTCTCTC 18105
Qy 206 GGTTCACCTGCCATGTCTTACTACTTTGACGCGCATGATGGCTTTGAAGAACTTGC 265
Db 18106 CATTTACCTGGCGGTCTACTTTGACAGCCGATGATGGCTTTGAAGAACTTGC 18165
Qy 266 CAAATACCTTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 18166 CAAATACCTTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 18225
Qy 326 CGAGAACCAACGAGTGGCGGATCTTCTTCAGGATATCAAGAACAGACTGTGATG- 384
Db 18226 GTAGAACCAACGAGTGGCGGATCTTCTTCAGGATATCAAGAACAGACTGTGCGGG 18285
Qy 385 -----ACTGGGAGCGGCTGAATGCAATG-----AG 413
Db 18286 GAGATGCGATGGGAGCGGCTGAATGCGATGATACATTTGGAAAAAATGTGCGAT 18345
Qy 414 TGTGCATTACATTTGGAAAAAATGTGAATCAGTCAGTCATCTGGAATTC 462
Db 18346 TTTGCATTACATTTGGAAAAAATGTGAATCAGTCAGTCATCTGGAATTC 18394

RESULT 13

US-09-313-294A-6635
; Sequence 6635, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6635
; LENGTH: 292
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700352138H1
US-09-313-294A-6635

Query Match 26.6%; Score 237.2; DB 4; Length 292;

Best Local Similarity 98.8%; Pred. No. 9.7e-65; Mismatches 3; Indels 0; Gaps 0;

Matches 239; Conservative 0;

Qy 221 GTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGCCAAATCTTTCTTCA 280
Db 1 GTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGCCAAATCTTTCTTCA 60
Qy 281 CCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGG 340
Db 61 CCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGG 120
Qy 341 TGGCGAATCTCTTCCAGGATATCAAGAACCAAGACTGTGATCAGTGGAGAGCGGCT 400
Db 121 TGGCGAATCTCTTCCAGGATATCAAGAACCAAGACTGTGATCAGTGGAGAGCGGCT 180
Qy 401 GAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCAGTCACCTCTGGAATT 460
Db 181 GAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCAGTCACCTCTGGAATT 240
Qy 461 CC 462
Db 241 GC 242

RESULT 14

US-09-949-016-115137/c
; Sequence 115137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115137
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-115137

Query Match 25.3%; Score 225.4; DB 4; Length 601;
Best Local Similarity 95.5%; Pred. No. 8.2e-61;
Matches 232; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 86 CGCCTCTCTTCTAGTGGCGGCATGACGACCGCGTCCACCTGCGCAGGTGCGCCAGAACTA 145
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QY 146 CCACGAGACTCAGAGGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 205
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Db 184 CCACGAGACTCAGAGGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 125
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QY 206 CGTTTACCTGTCCATGTCTTACTCTTTGACCGCGATGATGGCTTTTGAAGAACTTTGC 265
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QY 266 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
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Db 64 CACATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 5
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QY 326 GCA 328
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Db 4 GCA 2

RESULT 15
US-09-640-173-7
; Sequence 7, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-640-173-7

Query Match 24.9%; Score 222; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.6e-60;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CGCCTCTCTTCTAGTGGCGGCATGACGACCGCGTCCACCTGCGCAGGTGCGCCAGAACTA 145
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QY 146 CCACGAGACTCAGAGGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 205
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Db 235 CCACGAGACTCAGAGGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 294
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QY 206 CGTTTACCTGTCCATGTCTTACTCTTTGACCGCGATGATGGCTTTTGAAGAACTTTGC 265
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Db 295 CGTTTACCTGTCCATGTCTTACTCTTTGACCGCGATGATGGCTTTTGAAGAACTTTGC 354
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QY 266 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGC 307
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Db 355 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGC 396
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Search completed: April 1, 2005, 13:09:31
Job time : 143 sec

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		Match	Length			
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2	864.8	97.1	891	6	AX023293	Sequence
3	845	94.8	845	5	AY033611	Homo sapi
4	373.8	42.0	567	6	AX381667	Sequence
5	373.8	42.0	708	9	AF088851	Homo sapi
6	373.8	42.0	737	9	HUMFERHA	Human ferri
7	373.8	42.0	788	9	BC015156	Homo sapi
8	373.8	42.0	790	6	BD094093	Shear str
9	373.8	42.0	790	9	HUMFERH	Human ferri
10	373.8	42.0	801	6	CQ834024	Sequence
11	373.8	42.0	801	9	HSAPFI1	Human mRNA
12	373.8	42.0	804	6	CQ729634	Sequence
13	373.8	42.0	856	9	BC070494	Homo sapi
14	373.8	42.0	884	9	BC016857	Homo sapi
15	373.8	42.0	900	6	BC001399	Homo sapi
16	373.8	42.0	920	6	AX020273	Sequence
17	373.8	42.0	923	9	BC000857	Homo sapi
18	373.8	42.0	924	9	BC073750	Homo sapi
19	373.8	42.0	925	9	BC013724	Homo sapi

REFERENCE 1 (bases 1 to 845)
 Moroz, C., Traub, L., Maymon, R. and Zahalka, M.A.
 TITLE PLIF, a novel human ferritin subunit from placenta with
 immunosuppressive activity
 J. Biol. Chem. 277 (15), 12901-12905 (2002)
 MEDLINE 21935397
 PUBMED 11821435
 REFERENCE 2 (bases 1 to 845)
 Moroz, C.
 TITLE Direct Submission
 JOURNAL Submitted (29-APR-2001) Molecular Immunology, Pelsenstein Medical
 Research Center, Rabin Medical Center, Beilinson Campus,
 Petah-Tikva 49100, Israel
 FEATURES Location/Qualifiers
 source 1..845
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /chromosome="1"
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 DVALKNPAKYFLQSHREHAEKLMKLNQGRGRIFLODIKPKDCDDWESGLNAME
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 IFRSP"
 misc_feature 417..845
 /note="similar to mitochondrial sequence, but present in
 PLIF transcripts from placenta and several other sources"
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 Query Match 94.8%; Score 845; DB 9; Length 845;
 Best Local Similarity 100.0%; Pred. No. 2.1e-212;
 Matches 845; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 47 AATTCCAAAAATGTAATGCACATCCATTCGATTCAGCGCGCTCTCTTAGTCGCGC 106
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 QY 1 AATTCCAAAAATGTAATGCACATCCATTCGATTCAGCGCGCTCTCTTAGTCGCGC 60
 DB |||||
 QY 107 CATGACGACCGCTCCACCTCGAGTGGCGGCGACAGTACCACAGGACTCAGAGGCGC 166
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 QY 61 CATGACGACCGCTCCACCTCGAGTGGCGGCGACAGTACCACAGGACTCAGAGGCGC 120
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 QY 167 CATCAACCGCAGATCAACCTGGAGCTCTACGCCCTCTACCTGTTCATGTCCTTA 226
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 QY 121 CATCAACCGCAGATCAACCTGGAGCTCTACGCCCTCTACCTGTTCATGTCCTTA 180
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 QY 227 CTACTTTGACCGGATGATGGCTTTGAAGAACTTTCGCAAACTTCTTCCAAATC 286
 DB |||||
 QY 181 CTACTTTGACCGGATGATGGCTTTGAAGAACTTTCGCAAACTTCTTCCAAATC 240
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 QY 287 TCATGAGAGAGGGAACATGCTGAGAACTCATGAAGCTGAGAGTCCAGAACCAAGGTCGCG 346
 DB |||||
 QY 241 TCATGAGAGAGGGAACATGCTGAGAACTCATGAAGCTGAGAGTCCAGAACCAAGGTCGCG 300
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 QY 407 AATGAGTGTGATTAACATTTGGAAAAAATGTGAATCAGTCACTTCTGGAATTCCTTC 466
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 QY 467 TCCTATCTCTCCAGTCTAGTGTGTCATCACTATACCTACTACACAGCGCACTCA 526
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 QY 721 CTACACTTATCATCTTCAAAATTCCTTACTGACTATCTCTGAAATCGCTGCGCT 780
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 QY 887 AAAAA 891
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 QY 841 AAAAA 845
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 RESULT 4
 AX381667
 LOCUS AX381667 567 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 605 from Patent WO0212280.
 ACCESSION AX381667
 VERSION AX381667.1 GI:19576489
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Pyle, R.A., Xu, J. and Secrist, H.
 TITLE Compositions and methods for the therapy and diagnosis of colon
 cancer
 JOURNAL Patent: WO 0212280-A 605 14-FEB-2002;
 CORIXA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..567
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 42.0%; Score 373.8; DB 6; Length 567;
 Best Local Similarity 99.5%; Pred. No. 9.4e-88;
 Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 86 CCGCTCTCTTACTCGCGCCATGACGACCGCTCCACCTCGAGGTGCGCCAGAACTA 145
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 QY 138 CCGCTCTCTTACTCGCGCCATGACGACCGCTCCACCTCGAGGTGCGCCAGAACTA 197
 DB |||||
 QY 146 CCACGAGCTCAGAGCGCGCATCAACCGCCAGATCAACCTGAGCTCTACGCTCCTA 205
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 QY 198 CCACGAGCTCAGAGCGCGCATCAACCGCCAGATCAACCTGAGCTCTACGCTCCTA 257
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 QY 206 CGTTTACTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 265
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 QY 258 CGTTTACTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 317
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 QY 266 CAATACTTTCTTCCCAATCTCATGAGGAGGGAACATCTGAGAACTGATGAAGCT 325
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 QY 326 GCAGAACCAACGAGGTGCGGAATCTTCTTTCAGGATATCAAGAAACACAGACTGTGATGA 385
 DB |||||
 QY 378 GCAGAACCAACGAGGTGCGGAATCTTCTTTCAGGATATCAAGAAACACAGACTGTGATGA 437
 DB |||||

Qy 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 438 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 497
Qy 446 GTCACTACTGGAATTC 462
Db 498 GTCACTACTGGAATTC 514

RESULT 5
AF088851 708 bp mRNA linear PRI 01-AUG-2000
LOCUS Homo sapiens ferritin heavy chain subunit mRNA, complete cds.
DEFINITION AF088851
ACCESSION AF088851.1 GI:9621743
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 708)
AUTHORS Franco,A.V., Gray,C.P., Myers,K. and Hersey,P.
TITLE Detection of ferritin heavy chain by serex: A multifunctional molecule in malignant tumour cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 708)
AUTHORS Franco,A.V., Gray,C.P., Myers,K. and Hersey,P.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1998) Oncology and Immunology, Royal Newcastle Hospital, Cnr King and Watt Streets, Newcastle, N.S.W 2300, Australia

FEATURES
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ORIGIN
Query Match 42.0%; Score 373.8; DB 9; Length 708;
Best Local Similarity 99.5%; Pred. No. 9.8e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 86 CCGCTCTCTTGTAGTCGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
Db 21 CCGCTCTCTTGTAGTCGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 80
Qy 146 CCACAGGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
Db 81 CCACAGGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 140
Qy 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTGC 265
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Qy 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 321 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 380
Qy 446 GTCACTACTGGAATTC 462
Db 381 GTCACTACTGGAATTC 397

RESULT 6
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LOCUS Human ferritin heavy subunit mRNA, complete cds.
DEFINITION HUMFERHA
ACCESSION M12937
VERSION M12937.1 GI:182506
KEYWORDS ferritin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 737)
AUTHORS Chou,C.C., Gatti,R.A., Fuller,M.L., Concannon,P., Wong,A.,
Chada,S., Davis,R.C. and Salser,W.A.
TITLE Structure and expression of ferritin genes in a human promyelocytic cell line that differentiates in vitro
JOURNAL Mol. Cell. Biol. 6 (2), 566-573 (1986)
MEDLINE 87064341
PUBMED 3023856
COMMENT Original source text: Human promyelocytic cell line HL-60 cDNA to mRNA, clone HL217.

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Location/Qualifiers
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ORIGIN
Query Match 42.0%; Score 373.8; DB 9; Length 737;
Best Local Similarity 99.5%; Pred. No. 9.8e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 86 CCGCTCTCTTGTAGTCGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
Db 5 CCGCTCTCTTGTAGTCGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 64
Qy 146 CCACAGGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205
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QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGCAATCA 445
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 Db 365 CTCACACTGGAATGCC 381
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RESULT 7
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 LOCUS Homo sapiens ferritin, heavy polypeptide 1, mRNA (cdna clone
 DEFINITION MGC:10010 IMAGE:3883694), complete cds.
 ACCESSION BC015156
 VERSION BC015156.1 GI:15929450
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 788)

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Heintz, E., Kettner, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932

JOURNAL
 MEDLINE
 PUBMED
 2 (bases 1 to 788)
 Strausberg, R.
 Direct Submission
 Submitted (01-OCT-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: DCTD/DP/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

REMARK
 COMMENT Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 22 Row: a Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES
 source

Location/Qualifiers
 1..788

gene

CDS

misc_feature

ORIGIN

Query Match 42.0%; Score 373.8; DB 9; Length 788;
 Best Local Similarity 99.5%; Pred. No. 9.9e-88;
 Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 86 CCGCTCTCTTGTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGACTA 145
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 Db 397 GTCACTACTGGAATGCC 413
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RESULT 8
 BD094093
 LOCUS Shear stress-responsive DNAs.
 DEFINITION BD094093
 ACCESSION BD094093.1 GI:22639681
 VERSION BD094093.1
 KEYWORDS WO 0125427-A/54.

BD094093 790 bp DNA linear PAT 27-AUG-2002

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 790)
AUTHORS     Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
            Notjima,H., Yoshihisa,H., Obayashi,M., Ota,T., Kawabata,A.,
            Sakurada,K., Kuga,T., Sekine,S., Nakamura,Y. and Sugan,S.
TITLE       Shear stress-responsive DNAs
JOURNAL     Patent: WO 0125427-A 54 12-APR-2001;
            KYOWA HAKKO KOGYO CO LTD,HIROSHI NOJIMA,HAJIME YOSHISUE, MASAYA
            OYAYASHI, TOSHIO OTA,AYAKO KAWABATA,KAZUHIRO SAKURADA,TETSURO KUGA,
            SUSUMU SEKINE, YUSUKE NAKAMURA,SUMIO SUGANO
COMMENT     OS Homo sapiens (human)
            PN WO 0125427-A/54
            PD 12-APR-2001
            PF 02-OCT-2000 WO 2000JP006840
            PR 01-OCT-1999 JP 99P 280976
            PI HIROSHI NOJIMA,HAJIME YOSHISUE,MASAYA OYAYASHI,TOSHIO OTA, PI
            AYAKO KAWABATA,
            PI KAZUHIRO SAKURADA,TETSURO KUGA,SUSUMU SEKINE,YUSUKE NAKAMURA,
            SUMIO SUGANO
            PC C12N15/12,C07K14/435,C07K16/18,C12P21/02,C12Q1/68,A61K38/00,
            A61K39/395,
            PC A61K48/00,A61P9/10,G01N33/50,G01N33/53
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Best Local Similarity 99.5%; Pred. No. 9.9e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGCCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
DB 56 CGCGCTCTCTTCTAGTCGGCGCCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 115
QY 146 CCACGAGACTCAGAGGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 205
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QY 206 CGTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 265
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QY 446 GTCACTACTGGAATTC 462
DB 416 GTCACTACTGGAATTC 432

RESULT 9
HUMFERH HUMFERH 790 bp mRNA linear PRI 08-NOV-1994
LOCUS Human ferritin H chain mRNA, complete cds.
DEFINITION M1146
ACCESSION M1146
VERSION M1146.1 GI:182504

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ferritin.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 790)
AUTHORS     Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
            Boyd,D., Vecoli,C., Belcher,D.M., Jain,S.K. and Drysdale,J.W.
            Structural and functional relationships of human ferritin H and L
            chains deduced from cDNA clones
JOURNAL     J. Biol. Chem. 260 (21), 11755-11761 (1985)
MEDLINE     86008223
PUBMED      3840162
COMMENT     Original source text: Human liver, cDNA to mRNA, clone pHF16.
            Draft entry, computer-readable and printed copy of sequences in [1]
            kindly provided by J.Drysdale, 29-JAN-1986.

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ORIGIN      148 bp upstream of Sau3A site.
Query Match 42.0%; Score 373.8; DB 9; Length 790;
Best Local Similarity 99.5%; Pred. No. 9.9e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGCCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
DB 56 CGCGCTCTCTTCTAGTCGGCGCCATGACGACGCGCTCCACCTCGCAGGTGGCCGAGAACTA 115
QY 146 CCACGAGACTCAGAGGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 205
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QY 206 CGTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 265
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DB 416 GTCACTACTGGAATTC 462

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Db 416 GTCACCTACTGGAAGTGC 432

RESULT 10
LOCUS Q0834024
DEFINITION Sequence 60 from Patent EP1439393.
ACCESSION Q0834024
VERSION Q0834024.1 GI:50833629
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Asle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J.,
Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.E., Maimonis, P.J.,
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and
Molino, G.A.
TITLE Detection methods using TIMP 1 for colon cancer diagnosis
JOURNAL Patent: EP 1439393-A 60 21-JUL-2004;
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
AND RESEARCH (US)

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Best Local Similarity 99.5%; Pred. No. 1e-87; Indels 0; Gaps 0;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTCTTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
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QY 446 GTCACCTACTGGAATTC 462
DB 430 GTCACCTACTGGAAGTGC 446

RESULT 11
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LOCUS Human mRNA for apoferritin H chain type.
DEFINITION X00318
ACCESSION X00318.1 GI:28434
VERSION apoferritin.
KEYWORDS apoferritin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 801)
Costanzo, F., Santoro, C., Colantuoni, V., Bensi, G., Raugei, G.,
Romano, V. and Cortese, R.
TITLE Cloning and sequencing of a full length cDNA coding for a human
apoferritin H chain: evidence for a multigene family
EMBO J. 3 (1), 23-27 (1984)
JOURNAL 84158535
MEDLINE 6323167
PUBMED
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Query Match 42.0%; Score 373.8; DB 9; Length 801;
Best Local Similarity 99.5%; Pred. No. 1e-87; Indels 0; Gaps 0;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTCTTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
DB 70 CCGCTCTCTCTTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 129

QY 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 205
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QY 266 CAAATACCTTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
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QY 326 GCAGAACCAACGAGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
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QY 386 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTAATCA 445
DB 370 CTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTAATCA 429

QY 446 GTCACCTACTGGAATTC 462
DB 430 GTCACCTACTGGAAGTGC 446

RESULT 12
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LOCUS Sequence 15568 from Patent WO02068579.
DEFINITION CQ729634
ACCESSION CQ729634
VERSION CQ729634.1 GI:42301253
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL

Patent: WO 02068579-A 15568 06-SEP-2002;

PE Corporation (NY) (US)

Location/Qualifiers

1. .804

/organism="Homo sapiens"

/mol_type="unassigned DNA"

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ORIGIN

Query Match 42.0%; Score 373.8; DB 6; Length 804;

Best Local Similarity 99.5%; Pred. No. 1e-87;

Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCCTTAGTCGCGCGCATGACGACGCGCTCCACCTCGCAGGTGCGCCAGAACTA 145

Db 70 CCGCTCTCCTTAGTCGCGCGCATGACGACGCGCTCCACCTCGCAGGTGCGCCAGAACTA 129

QY 146 CCACGAGGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 205

Db 130 CCACGAGGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 189

QY 206 CGTTTACCTGTCATGCTTACTTACTTTCGCGGATGATGCTTTCGAGAACTTTGTC 265

Db 190 CGTTTACCTGTCATGCTTACTTACTTTCGCGGATGATGCTTTCGAGAACTTTGTC 249

QY 266 CAATACCTTCTTCCACCAATCTCATGAGGAGGAGGAACATGCTGAGAACTGATGAAGCT 325

Db 250 CAATACCTTCTTCCACCAATCTCATGAGGAGGAGGAACATGCTGAGAACTGATGAAGCT 309

QY 326 GCAGAACCAACGAGGTGCGCGAATCTTCTTCCAGGATATCAAGAACAGACTGTGATGA 385

Db 310 GCAGAACCAACGAGGTGCGCGAATCTTCTTCCAGGATATCAAGAACAGACTGTGATGA 369

QY 386 CTGGAGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATCA 445

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QY 446 GTCACTACTGGAATTC 462

Db 430 GTCACTACTGGAATTC 446

RESULT 13

BC070494

LOCUS

DEFINITION

Homo sapiens ferritin, heavy polypeptide 1, mRNA (cdna clone

IMAGE:6009374), partial cds.

BC070494.1 GI:47125325

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 856)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 856)

Strausberg, R.

Direct Submission

Submitted (10-MAY-2004) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-rc@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@hgr.nih.gov

Anter, N., Ayete, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,

Tourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 174 Row: e Column: 18

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 4503794.

FEATURES

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/clones="IMAGE:6009374"

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ACCESSION BC016857
VERSION BC016857.1 GI:16877183
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
MEDLINE
PUBMED
12477932
REFERENCE 2 (bases 1 to 884)
Strausberg,R.
Direct Submission
TITLE
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-sbgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IPAK Plate: 20 Row: j Column: 8
This clone was selected for full length sequencing because it
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Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION	BC001399				
VERSION	BC001399.2				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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AUTHORS	Strausberg,R.I., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Udutin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Vialalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schin,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 900)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
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COMMENT	On Aug 19, 2003 this sequence version replaced gi:12655094.				
	Contact: MGC help desk				
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	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),				
	Gaithersburg, Maryland;				
	Web site: http://www.nisc.nih.gov/				
	Contact: nisc_mgc@nigri.nih.gov				
	Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,				

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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US-09-786-867C-1

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45	342.8	38.5	411	14	US-10-060-036-274	Sequence 274, App

ALIGNMENTS

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; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 605
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: n = A,T,C or G
; US-09-919-580-605

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US-09-918-995-27591
; Sequence 27591, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27591
; LENGTH: 583

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(583)
; OTHER INFORMATION: n = A,T,C or G
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US-10-278-698-128
; Sequence 128, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:

; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupt, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 128
; LENGTH: 790

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-128

Query Match 42.0%; Score 373.8; DB 19; Length 790;
Best Local Similarity 99.5%; Pred. No. 2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 86 CGCCTCTCTTACTGCGCGCATGACACCGCGTCCACCTCGCAGGTGCGCAGAACTA 145
Db 56 CGCCTCTCTTACTGCGCGCATGACACCGCGTCCACCTCGCAGGTGCGCAGAACTA 115
Qy 146 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCCTA 205
Db 116 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCCTA 175
Qy 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCATGATGGCTTTGAGAACTTTGC 265
Db 176 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCATGATGGCTTTGAGAACTTTGC 235
Qy 266 CAAATACCTTTCTTACCCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 236 CAAATACCTTTCTTACCCTCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 295
Qy 326 GCAGAACCAACGAGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 296 GCAGAACCAACGAGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 355
Qy 386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTATTTGGAAAAAATGTGAATCA 445
Db 356 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTATTTGGAAAAAATGTGAATCA 415
Qy 446 GTCACTACTGGAATTCC 462
Db 416 GTCACTACTGGAAGTGC 432

RESULT 4

US-10-278-698-644
; Sequence 644, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:

; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupt, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698

Db	Seq	Score	DB 19	Length	790	Mismatches	Conservative	Indels	Gaps	0
Qy	86	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	145					
Db	56	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	115					
Qy	146	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	205						
Db	116	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	175						
Qy	206	CGTTACCTGT	CCATGCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC	265						
Db	176	CGTTACCTGT	CCATGCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC	235						
Qy	266	CAAACTACTT	TTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCT	325						
Db	236	CAAACTACTT	TTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCT	295						
Qy	326	GCAGAACCAAC	GAGGTGGCGAATCTTCTTCAGGATATCAAGAAACCCAGACTGTGATGA	385						
Db	356	CTGGGAGACGG	GCTGNAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA	415						
Qy	446	GTCACCTACT	GGAATTC 462							
Db	416	GTCACCTACT	GGAATTC 432							

RESULT 5

US-10-734-564-60

Sequence 60, Application US/10734564

Publication No. US20040157278A1

GENERAL INFORMATION:

APPLICANT: Christopher C Burgess et al

TITLE OF INVENTION: Detection Methods Using TIMP1

FILE REFERENCE: 1657/2012

CURRENT APPLICATION NUMBER: US/10/734,564

CURRENT FILING DATE: 2003-12-12

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 60

LENGTH: 801

TYPE: DNA

ORGANISM: Homo sapiens

US-10-734-564-60

Query Match

Best Local Similarity 99.5%; Pred. No. 2e-110;

Mismatches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db	Seq	Score	DB 18	Length	801	Mismatches	Conservative	Indels	Gaps	0
Qy	86	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	145					
Db	70	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	129					
Qy	146	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	205						
Db	130	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	189						
Qy	206	CGTTACCTGT	CCATGCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC	265						

RESULT 6

US-10-198-846-9581

Sequence 9581, Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9581

LENGTH: 830

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 795, 801, 809

OTHER INFORMATION: n = A, T, C or G

US-10-198-846-9581

Query Match

Best Local Similarity 99.5%; Pred. No. 2e-110;

Mismatches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db	Seq	Score	DB 14	Length	830	Mismatches	Conservative	Indels	Gaps	0
Qy	86	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	145					
Db	56	CGGCTCTCTT	AGTGC	CGCCCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAGAACTA	115					
Qy	146	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	205						
Db	116	CCACGAGGACT	CAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA	175						
Qy	206	CGTTACCTGT	CCATGCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC	265						
Db	176	CGTTACCTGT	CCATGCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC	235						
Qy	266	CAAACTACTT	TTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCT	325						
Db	236	CAAACTACTT	TTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCT	295						
Qy	326	GCAGAACCAAC	GAGGTGGCGAATCTTCTTCAGGATATCAAGAAACCCAGACTGTGATGA	385						
Db	296	GCAGAACCAAC	GAGGTGGCGAATCTTCTTCAGGATATCAAGAAACCCAGACTGTGATGA	355						

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QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 356 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 415
QY 446 GTCACTACTGGAATGCC 462
Db 416 GTCACTACTGGAATGCC 432

RESULT 7
US-10-384-496-1
; Sequence 3, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakamur, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 3
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-231A-3

Query Match 42.0%; Score 373.8; DB 9; Length 920;
Best Local Similarity 99.5%; Pred. No. 2.1e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 173 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 232
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
Db 233 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 292
QY 206 GTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 265
Db 293 GTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 352
QY 266 CAATACTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 353 CAATACTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 412
QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 413 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 472
QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 473 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 532
QY 446 GTCACTACTGGAATGCC 462
Db 533 GTCACTACTGGAATGCC 549

RESULT 8
US-10-384-496-1
; Sequence 1, Application US/10384496
; Publication No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: AHRENS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND
; FILE REFERENCE: CMV-001.01
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; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-496-1

Query Match 42.0%; Score 373.8; DB 17; Length 955;
Best Local Similarity 99.5%; Pred. No. 2.2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 189 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 248
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
Db 249 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 308
QY 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 265
Db 309 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAAGAACTTTGC 368
QY 266 CAATACTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 369 CAATACTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 428
QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 429 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 488
QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 489 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 548
QY 446 GTCACTACTGGAATGCC 462
Db 549 GTCACTACTGGAATGCC 565

RESULT 9
US-10-071-766-9
; Sequence 9, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Huel-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 1138151.17
US-10-071-766-9

Query Match 42.0%; Score 373.8; DB 13; Length 998;
Best Local Similarity 99.5%; Pred. No. 2.2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 212 CGCGCTCTCCTTAGTCGCGCCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 271
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Qy	146	CCACCAGGACTCAGAGCGCGGCATCAACGCCCAGATCAA	CTTGAGGTCTTACGGCTCCTA	205
Db	272	CCACCAGGACTCAGAGCGCGCATCAACGCCCAGATCAAC	CTTGAGGTCTTACGGCTCCTA	331
Qy	206	CGTTTACCTGTCATGTCTTACTCTTTGACCGCGATGATG	TGCTTGTGAAGA	265
Db	332	CGTTTACCTGTCATGTCTTACTCTTTGACCGCGATGATG	TGCTTGTGAAGA	391
Qy	266	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGACA	CATGCTGAGAAA	325
Db	392	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGACA	CATGCTGAGAAA	451
Qy	326	GCAGAACCAACGAGGTGGCGGAATCTTCCITTCAGGAT	ATCAAGAAAA	385
Db	452	GCAGAACCAACGAGGTGGCGGAATCTTCCITTCAGGAT	ATCAAGAAAA	511
Qy	386	CTGGGAGAGCGGCTGAAATGC	AATGGAGTGTGCATTACATTTGGAAAAA	445
Db	512	CTGGGAGAGCGGCTGAAATGC	AATGGAGTGTGCATTACATTTGGAAAAA	571
Qy	446	GTCACTACTGGAATTC	462	
Db	572	GTCACTACTGGAATTC	588	

RESULT

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RESUL 10
US-10-071-766-10
; Sequence 10, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Hwei-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 1138151.1
US-10-071-766-10

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Query Match	42.0%	Score 373.8;	DB 13;	Length 1326;
Best Local Similarity	99.5%;	Pred. No. 2.6e-110;		
Matches 375;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	86	CCGCGCTCTCTTAGTTCGGCGGCATGACGACCGGTCCACCTCGCGAGGTGCGCGCAGAACTA	145	
Db	136	CCGCGCTCTCTTAGTTCGGCGGCATGACGACCGGTCCACCTCGCAGGTGCGCGCAGAACTA	195	
Qy	146	CCACGAGGACTCAGAGGCGGCCATCAACGGCCAGATCAACTGGAGCTCTAGGCTCTCTA	205	
Db	196	CCACGAGGACTCAGAGGCGGCCATCAACGGCCAGATCAACTGGAGCTCTAGGCTCTCTA	255	
Qy	206	CGTTTTACTGTGCCATGCTTTACTACTTTTGACCGGATGATGTGGCTTTTGAAGAACTTTGC	265	
Db	256	CGTTTTACTGTGCCATGCTTTACTACTTTTGACCGGATGATGTGGCTTTTGAAGAACTTTGC	315	
Qy	266	CAAAATCTTTTCTTCAACCAATCTCATGAGGAGGGAACAATGCTGAGAAACTGATGAAGCT	325	
Db	316	CAAAATCTTTTCTTCAACCAATCTCATGAGGAGGGAACAATGCTGAGAAACTGATGAAGCT	375	
Qy	326	GCAGAAACCAACGAGGTGGCCGAATCTTCCCTTCAGGATATCAAGAAACCCAGACTGTGTATGA	385	
Db	376	GCAGAAACCAACGAGGTGGCCGAATCTTCCCTTCAGGATATCAAGAAACCCAGACTGTGTATGA	435	
Qy	386	CTGGGAGAGCGGGTGAAATCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA	445	

Db 436 CTGGGAGACGGGTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 495

Qy 446 GTCACTACTGGAATTCC 462
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Db 496 GTCACTACTGGAATGC 512
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RESULT 11

```

US-09-919-580-912
; Sequence 912, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secret, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 912
; LENGTH: 791
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 628, 662, 677, 703, 715, 741, 785, 786
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-912

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Query Match	41.9%	Score 373.4	DB 9	Length 791
Best Local Similarity	99.7%	Pred. No. 2.6e-110		
Matches 374	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	86	CCGCGCTCTCTTAGTTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA	145	
Db	180	CCGCGCTCTCTTAGTTCGGCGGCATGACGACCGGTCCACCTCGCAGGTGCGCCAGAACTA	239	
Qy	146	CCACGAGACTCAGAGGCGGCCATCAACCGCCAGATCAACTGAGAGCTCTACGCTCTCTA	205	
Db	240	CCACGAGACTCAGAGGCGGCCATCAACCGCCAGATCAACTGAGAGCTCTACGCTCTCTA	299	
Qy	206	CGTTTACTGTCCATGCTTACTACTTTGACCGGAGATGCTGGCTTTGAGAACTTTGC	265	
Db	300	CGTTTACTGTCCATGCTTACTACTTTGACCGGAGATGCTGGCTTTGAGAACTTTGC	359	
Qy	266	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGGAAATGCTCAGAGAACTGATGAAGCT	325	
Db	360	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGGAAATGCTCAGAGAACTGATGAAGCT	419	
Qy	326	GCAGAAACCAACGAGGTGCCAAATCTTCTTCAGGATATCAAGAAACACGAGCTGTGATGA	385	
Db	420	GCAGAAACCAACGAGGTGCCAAATCTTCTTCAGGATATCAAGAAACACGAGCTGTGATGA	479	
Qy	386	CTGGGAGAGCGGCTGGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTCAATCA	445	
Db	480	CTGGGAGAGCGGCTGGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTCAATCA	539	
Qy	446	GTCACTACTGGAATTT	460	
Db	540	GTCACTACTGGAATTT	554	

RESULT, T 12.

RESUB 12
US-09-880-107-2174
; Sequence 2174, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe

```
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2174
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L20941
US-09-880-107-2174

Query Match          41.9%; Score 373; DB 9; Length 1198;
Best Local Similarity 98.7%; Pred. No. 4.5e-110;
Matches 376; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 CAGCCGCCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGA 141
Db 183 CCGCGGCCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGA 242

QY 142 ACTACACAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCT 201
Db 243 ACTACACAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCT 302

QY 202 CCTAGCTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGCTTTGAGAACT 261
Db 303 CCTAGCTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGCTTTGAGAACT 362

QY 262 TTGCCAAATACCTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGA 321
Db 363 TTGCCAAATACCTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGA 422

QY 322 AGCTCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTG 381
Db 423 AGCTCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTG 482

QY 382 ATGACTGGGAGGCGGGTGAATGCAATGGAGTGTGCATTACATTTGAAAAAATGTGA 441
Db 483 ATGACTGGGAGGCGGGTGAATGCAATGGAGTGTGCATTACATTTGAAAAAATGTGA 542

QY 442 ATCAGTCTACTGGAATTC 462
Db 543 ATCAGTCTACTGGAATTC 563

RESULT 13
US-10-425-115-12412
; Sequence 12412, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 12412
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: (1)..(882)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_1111315C.1.
US-10-425-115-12412

Query Match          41.8%; Score 372.8; DB 18; Length 882;
Best Local Similarity 99.2%; Pred. No. 4.4e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 CCGCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGAATA 145
Db 173 CCGCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGAATA 232

QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTA 205
Db 233 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTA 292

QY 206 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGCTTTGAAAGAACTTTGC 265
Db 293 CGTTTACCTGTCCATGTCTTACTACTTTTGACCGCGATGATGCTTTGAAAGAACTTTGC 352

QY 266 CAAATACCTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 353 CAAATACCTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 412

QY 326 GCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTGATGA 385
Db 413 GCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTGATGA 472

QY 386 CTGGGAGAGCGGGTGAATGCAATGGAGTGTGCATTACATTTGAAAAAATGTGAATCA 445
Db 473 CTGGGAGAGCGGGTGAATGCAATGGAGTGTGCATTACATTTGAAAAAATGTGAATCA 532

QY 446 GTCACTACTGGAATTC 462
Db 533 GTCACTACTGGAATTC 549

RESULT 14
US-09-919-580-889
; Sequence 889, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 889
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 675, 690, 711, 718, 742, 759
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-889

Query Match          41.8%; Score 372.2; DB 9; Length 776;
Best Local Similarity 99.2%; Pred. No. 6.4e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 CCGCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGAATA 145
Db 178 CCGCCTCTCTTAGTTCGCGCCCATGACGACCGGTCCACCTCGCAGGTGCGCCAGAATA 237

QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTA 205
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Db 238 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTACGCCCTCTA 297
Qy 206 GCTTTACCTGTCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 298 GCTTTACCTGTCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 357
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACAATGCTGAGAACTGATGAAGCT 325
Db 358 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACAATGCTGAGAACTGATGAAGCT 417
Qy 326 GCAGAACCAACGAGGTGGCGGAATCTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 418 GCAGAACCAACGAGGTGGCGGAATCTCTTCAGGATATCAAGAAACAGACTGTGATGA 477
Qy 386 CTGGGAGAGCGGGCTGAATGCAATCGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 445
Db 478 CTGGGAGAGCGGGCTGAATGCAATCGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 537
Qy 446 GTCACACTGGAATTC 462
Db 538 GTCACACTGGAATTC 554
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RESULT 15

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US-09-823-245A-42
; Sequence 42, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fichtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-42
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Query Match 41.8%; Score 372.2; DB 9; Length 900;
Best Local Similarity 99.2%; Pred No. 7e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACTCGCAGGTGGCCAGAACTA 145
Db 166 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACTCGCAGGTGGCCAGAACTA 225
Qy 146 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 205
Db 226 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 285
Qy 206 GCTTTACCTGTCATGCTTACTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 265
Db 286 GCTTTACCTGTCATGCTTACTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 345
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACAATGCTGAGAACTGATGAAGCT 325
Db 346 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACAATGCTGAGAACTGATGAAGCT 405
Qy 326 GCAGAACCAACGAGGTGGCGGAATCTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
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Db 406 GCAGAACCAACGAGGTGGCGGAATCTCTTCAGGATATCAAGAAACAGACTGTGATGA 465
Qy 386 CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 445
Db 466 CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 525
Qy 446 GTCACACTGGAATTC 462
Db 526 GTCACACTGGAATTC 542
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Search completed: April 1, 2005, 13:16:57
Job time : 438 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:27:22 ; Search time 2388 Seconds
(without alignments)
14202.372 Million cell updates/sec

Title: US-09-786-867C-1
Perfect score: 891
Sequence: 1 ttgacacagacccaactggc.....acgacacacataaaaaaa 891

Scoring table: IDENTITY NUC
GAPENT 10.0 , Gapent 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsei:*
9: gb_gsei2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	375.8	42.2	688	BG542331	BG542331 602571887
2	375.8	42.2	803	BU955418	BU955418 AGENCOURT
3	375.8	42.2	877	BUI70044	BUI70044 AGENCOURT
4	375	42.1	602	BI544288	BI544288 603241665
5	375	42.1	704	BE281505	BE281505 601155067
6	375	42.1	900	BE908934	BE908934 601497872
7	375	42.1	978	BE562266	BE562266 601344724
8	374.8	42.1	1001	BUI196441	BUI196441 AGENCOURT
9	374.6	42.0	575	BU073943	BU073943 in26e12.y
10	374.6	42.0	788	BGI63468	BGI63468 602338464
11	374.6	42.0	875	BF983589	BF983589 602306579
12	374.6	42.0	942	BE740697	BE740697 601593667
13	374.6	42.0	953	BF976359	BF976359 602244490
14	374.2	42.0	507	BQ637251	BQ637251 he07f05.y
15	374.2	42.0	579	BP214869	BP214869 BP214869
16	374.2	42.0	582	BP214989	BP214989 BP214989
17	374.2	42.0	582	BP228811	BP228811 BP228811
18	374.2	42.0	582	BP353301	BP353301 BP353301
19	374.2	42.0	583	BP295488	BP295488 BP295488
20	374.2	42.0	642	CF128424	CF128424 UI-HF-ET0
21	374.2	42.0	697	CF128432	CF128432 UI-HF-ET0
22	374.2	42.0	726	CF131121	CF131121 UI-HF-ET0
23	374.2	42.0	772	CF131109	CF131109 UI-HF-ET0
24	374.2	42.0	773	BQ219393	BQ219393 AGENCOURT

25	374.2	42.0	817	2	BF576393	BF576393 602134292
26	374.2	42.0	952	4	BG331712	BG331712 602433128
27	374	42.0	567	5	BP234849	BP234849 BP234849
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29	374	42.0	582	5	BP231281	BP231281 BP231281
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31	374	42.0	582	5	BP352853	BP352853 BP352853
32	374	42.0	583	5	BP214599	BP214599 BP214599
33	374	42.0	583	5	BP231792	BP231792 BP231792
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35	373.8	42.0	456	5	BP232703	BP232703 BP232703
36	373.8	42.0	458	4	BM686184	BM686184 UI-E-CR0-
37	373.8	42.0	461	5	BQ316932	CM0-CT034
38	373.8	42.0	484	1	AJ705380	AJ705380 AJ705380
39	373.8	42.0	484	5	BP234848	BP234848 BP234848
40	373.8	42.0	485	6	CB751823	CB751823 TgESTzyHS
41	373.8	42.0	485	7	NS2504	NS2504 yv52a11.s1
42	373.8	42.0	497	2	BF724302	BF724302 bx03c06.y
43	373.8	42.0	508	2	BF727248	BF727248 by18h05.y
44	373.8	42.0	515	5	BM887644	BM887644 TM231 Hum
45	373.8	42.0	517	4	BM798732	BM798732 K-EST0082

ALIGNMENTS

RESULT 1
BG542331
LOCUS
DEFINITION BG542331 688 bp mRNA linear EST 03-APR-2001
602571887F1 NIH_MGC_77 Homo sapiens cdna clone IMAGE:4696508 5',
mRNA sequence.
ACCESSION BG542331
VERSION BG542331.1 GI:13534564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI523 row: m column: 21
High quality sequence stop: 679.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4696508"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: sfii (ggccattggcc); Site 2: sfii (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 Kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.2%; Score 375.8; DB 4; Length 688;
 Best Local Similarity 97.0%; Pred. No. 3.9e-98;
 Matches 383; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 68 CACTCCATTGATTCAGCCGCGCTCTCTTAGTCGCGCCATGAGCAGCGGTCACCTC 127
 DB 101 CCCTCCGTCACCTCTTTCGCGCGCTCTCTTAGTCGCGCCATGAGCAGCGGTCACCTC 160

QY 128 GCAGGTGGCCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCCGAGATCAACT 187
 DB 161 GCAGGTGGCCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCCGAGATCAACT 220

QY 188 GCAGTCTACGCTCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCT 247
 DB 221 GCAGTCTACGCTCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCT 280

QY 248 GCCTTTGAGAACTTGGCAATATCTTCTTCCACCAATCTATGAGGAGGAGACATGC 307
 DB 281 GCCTTTGAGAACTTGGCAATATCTTCTTCCACCAATCTATGAGGAGGAGACATGC 340

QY 308 TGAGAACTGTGATGAAGCTGCAGAACCAACAGGAGTGGCGCAATCTTCTTCCAGGATCA 367
 DB 341 TGAGAACTGTGATGAAGCTGCAGAACCAACAGGAGTGGCGCAATCTTCTTCCAGGATCA 400

QY 368 GAAACAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGATTAATTT 427
 DB 401 GAAACAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGATTAATTT 460

QY 428 GGAATAAATGTGAATCACTACTGTAATTC 462
 DB 461 GGAATAAATGTGAATCACTACTGTAATTC 495

RESULT 2
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 LOCUS
 DEFINITION AGENCOURT_10609097 NIH_MGC_126 Homo sapiens cDNA clone
 IMAGE:6727525 5', mRNA sequence.

ACCESSION BUI70044
 VERSION BUI70044.1 GI:24184990
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM3047 row: k column: 12
 High quality sequence stop: 542.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6727525"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC 126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

FEATURES
source

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

REFERENCE
 1 (bases 1 to 803)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM3047 row: k column: 12
 High quality sequence stop: 542.
 Location/Qualifiers
 1..803
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6727525"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC 126"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
 Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, parotid - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3',
 adaptors were used in cloning as follows:
 5'-AAGCAGTGTATCAACGAGATGCGCAATACGCGGG-3' and
 5'-ATTAGAGCGGCGGCGCATG-DT(30)NN-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the 0.5-1
 kb size fraction (other fractions present in NIH MGC 127
 and NIH MGC 128). Library created in the laboratory of T.
 Udels, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 42.2%; Score 375.8; DB 5; Length 803;
 Best Local Similarity 97.0%; Pred. No. 4e-98;
 Matches 383; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 68 CACTCCATTGATTCAGCCGCGCTCTCTTAGTCGCGCCATGAGCAGCGGTCACCTC 127
 DB 102 CCCTCCGTCACCTCTTTCACCGCGCTCTCTTAGTCGCGCCATGAGCAGCGGTCACCTC 161

QY 128 GCAGGTGGCCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCCGAGATCAACT 187
 DB 162 GCAGGTGGCCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCCGAGATCAACT 221

QY 188 GCAGTCTACGCTCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCT 247
 DB 222 GCAGTCTACGCTCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCTAGTTCCT 281

QY 248 GCCTTTGAGAACTTGGCAATATCTTCTTCCACCAATCTATGAGGAGGAGACATGC 307
 DB 282 GCCTTTGAGAACTTGGCAATATCTTCTTCCACCAATCTATGAGGAGGAGACATGC 341

QY 308 TGAGAACTGTGATGAAGCTGCAGAACCAACAGGAGTGGCGCAATCTTCTTCCAGGATCA 367
 DB 342 TGAGAACTGTGATGAAGCTGCAGAACCAACAGGAGTGGCGCAATCTTCTTCCAGGATCA 401

QY 368 GAAACAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGATTAATTT 427
 DB 402 GAAACAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGATTAATTT 461

QY 428 GGAATAAATGTGAATCACTACTGTAATTC 462
 DB 462 GGAATAAATGTGAATCACTACTGTAATTC 496

RESULT 3
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LOCUS

DEFINITION AGENCOURT_7932964 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6009955
 5', mRNA sequence.

ACCESSION BUI70044

VERSION BUI70044.1 GI:22684028

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: DCTD/BTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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Plate: LLAM13194 row: k column: 04
High quality sequence stop: 643.
Location/Qualifiers
source 1. .877
FEATURES

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Query Match	42.2%;	Score 375.8;	DB 5;	Length 877;																		
Best Local Similarity	97.0%;	Pred. No. 4.1e-98;																				
Matches 383;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;																		
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QY	128	GC	AGT	GC	GC	CA	AA	CT	AC	CA	CG	AG	GC	CG	CCAT	CA	AC	CG	CG	CA	CT	187
DB	133	GC	AGT	GC	GC	CA	AA	CT	AC	CA	CG	AG	GC	CG	CCAT	CA	AC	CG	CG	CA	CT	192
QY	188	GG	AG	CT	CT	AC	GC	CT	CT	AG	TT	AC	CT	GT	CT	CA	TT	TG	AC	GG	AT	247
DB	193	GG	AG	CT	CT	AC	GC	CT	CT	AG	TT	AC	CT	GT	CT	CA	TT	TG	AC	GG	AT	252
QY	248	GG	CT	TT	GA	AG	AA	CT	TT	GG	CA	AA	CT	TT	TT	CA	CA	AA	CT	CA	TG	307
DB	253	GG	CT	TT	GA	AG	AA	CT	TT	GG	CA	AA	CT	TT	TT	CA	CA	AA	CT	CA	TG	312
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DB	373	GA	AA	CC	AG	AC	TG	TG	AT	GAC	TG	GG	AG	CG	GG	CT	CA	AT	TG	CA	AT	432
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DB	433	GG	AA	AAAA	AT	GT	GA	AT	CA	GT	CAC	TAC	TG	GA	AT	TCC						467

RESULT 4	
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DEFINITION	mRNA sequence.
ACCESSION	B1544288
VERSION	B1544288.1 GI:15431600
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 602) NTH-MGC http://mgc.nci.nih.gov/ .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov
COMMENT	Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11718 row: a column: 17
High quality sequence stop: 600.

Query Match	42.1%;	Score 375;	DB 4;	Length 602;
Best Local Similarity	97.4%;	Pred. No. 6.4e-98;		
Matches 381;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	72	CCATTGCAATTCAGCGCGCGCTCTCTTAGTCGCGCGCCATGACGACCGCGTCCACCTCGCAG	131	
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Qy	132	GTGCGCGAGAACTACCAACGAGGACTCAGAGGCGGCCATCAACCGCCAGATCAACCTGGAG	191	
Db	234	GTGCGCGAGAACTACCAACGAGGACTCAGAGGCGGCCATCAACCGCCAGATCAACCTGGAG	293	
Qy	192	CTCTACGCTCCTACGTTTACCTGTCCATGCTCTTACTCTTTCGACCGCGATGATGCGCT	251	
Db	294	CTCTACGCTCCTACGTTTACCTGTCCATGCTCTTACTCTTTCGACCGCGATGATGCGCT	353	
Qy	252	TTGAAGAACTTTGCCAAATACTTTCTTTCACCAATCTCATGAGGAGGGGAACATGCTGAG	311	
Db	354	TTGAAGAACTTTGCCAAATACTTTCTTTCACCAATCTCATGAGGAGGGGAACATGCTGAG	413	
Qy	312	AAACTGATGAAGCTGCGAAGCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAA	371	
Db	414	AAACTGATGAAGCTGCGAAGCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAA	473	
Qy	372	CCAGACTGTGATGACTGGGAGAGCGGCTCGAATGCAATGGAGTGTGCAATTACATTTCGAA	431	
Db	474	CCAGACTGTGATGACTGGGAGAGCGGCTCGAATGCAATGGAGTGTGCAATTACATTTCGAA	533	
Qy	432	AAAAATGTGAATCAGTCACTTACTGGAAATTC	462	
Db	534	AAAAATGTGAATCAGTCACTTACTGGAAATTC	564	

RESULT	5
BE281505	
LOCUS	
DEFINITION	601155067F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138449 5', linear mRNA 704 bp EST 13-JUL-2000
ACCESSION	BE281505
VERSION	BE281505.1 GI:9156525
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 704) NIH-MGC http://mgc.nci.nih.gov/ .

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM103 row: f column: 18
High quality sequence stop: 655.
Location/Qualifiers
1. .704
/organism="Homo sapiens"
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/clone="IMAGE:3138449"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source

Query Match 42.1%; Score 375; DB 2; Length 704;
Best Local Similarity 97.4%; Pred. No. 6.6e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 72 CCATTGCATTGACGGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 131
Db 120 CCACGCGCGCGCGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 179
QY 132 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 191
Db 180 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 239
QY 192 CTCTACGCTCTACGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCT 251
Db 240 CTCTACGCTCTACGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCT 299
QY 252 TTGAAGAACTTGGCCAAATCTCTTCCCAATCTCATGAGGAGGGAACATGCTGAG 311
Db 300 TTGAAGAACTTGGCCAAATCTCTTCCCAATCTCATGAGGAGGGAACATGCTGAG 359
QY 312 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 371
Db 360 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 419
QY 372 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 431
Db 420 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 479
QY 432 AAAAATGTGAATCACTCACTACTGGAATTC 462
Db 480 AAAAATGTGAATCACTCACTACTGGAATTC 510

ORIGIN

Query Match 42.1%; Score 375; DB 2; Length 704;
Best Local Similarity 97.4%; Pred. No. 6.6e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 72 CCATTGCATTGACGGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 131
Db 120 CCACGCGCGCGCGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 179
QY 132 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 191
Db 180 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 239
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Db 300 TTGAAGAACTTGGCCAAATCTCTTCCCAATCTCATGAGGAGGGAACATGCTGAG 359
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Db 360 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 419
QY 372 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 431
Db 420 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 479
QY 432 AAAAATGTGAATCACTCACTACTGGAATTC 462
Db 480 AAAAATGTGAATCACTCACTACTGGAATTC 510

RESULT 6
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DEFINITION mRNA sequence.
ACCESSION BE908934
VERSION BE908934.1 GI:10404009
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 900)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM9698 row: o column: 17
High quality sequence stop: 697.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:3900136"
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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."

FEATURES
source

Query Match 42.1%; Score 375; DB 2; Length 900;
Best Local Similarity 97.4%; Pred. No. 7.1e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 72 CCATTGCATTGACGGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 131
Db 150 CCACGCGCGCGCGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 209
QY 132 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 191
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QY 192 CTCTACGCTCTACGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCT 251
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QY 312 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 371
Db 390 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 449
QY 372 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 431
Db 450 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 509
QY 432 AAAAATGTGAATCACTCACTACTGGAATTC 462
Db 510 AAAAATGTGAATCACTCACTACTGGAATTC 540

ORIGIN

Query Match 42.1%; Score 375; DB 2; Length 900;
Best Local Similarity 97.4%; Pred. No. 7.1e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 72 CCATTGCATTGACGGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 131
Db 150 CCACGCGCGCGCGCGCTCTCCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 209
QY 132 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 191
Db 210 GTGCGCCAGAACTACACAGAGACTCAGAGGCGCGCATCAACCGCCAGATCAACTGGAG 269
QY 192 CTCTACGCTCTACGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCT 251
Db 270 CTCTACGCTCTACGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCT 329
QY 252 TTGAAGAACTTGGCCAAATCTCTTCCCAATCTCATGAGGAGGGAACATGCTGAG 311
Db 330 TTGAAGAACTTGGCCAAATCTCTTCCCAATCTCATGAGGAGGGAACATGCTGAG 389
QY 312 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 371
Db 390 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAA 449
QY 372 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 431
Db 450 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAATGCAATTTGAA 509
QY 432 AAAAATGTGAATCACTCACTACTGGAATTC 462
Db 510 AAAAATGTGAATCACTCACTACTGGAATTC 540

RESULT 7
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LOCUS 601344724F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677789 5';
DEFINITION mRNA sequence.
ACCESSION BE562266
VERSION BE562266.1 GI:9805986

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
cdna Library Preparation: Ling Hong/Rubin Laboratory
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM353 row: o column: 06
High quality sequence start: 4
High quality sequence stop: 812.
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    /clone_lib="NIH MGC 8"
    /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
    EcoRI; cdna made by oligo-dt priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Size-selected >500bp for average
    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 42.1%; Score 375; DB 2; Length 978;
Best Local Similarity 97.4%; Pred. No. 7.3e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 72 CCATTGCTTACCGCGCTCTCTTAGTCGCGGCATGACCGCGTCCACCTCGCAG 131
DB 182 CCACCGCGCGCGCGCTCTCTTAGTCGCGGCATGACCGCGTCCACCTCGCAG 241
QY 132 GTGCGCCAGAACTACACCGAGCTCAGAGCGCGCATCAACCGCGAGATCAACCTGGAG 191
DB 242 GTGCGCCAGAACTACACCGAGCTCAGAGCGCGCATCAACCGCGAGATCAACCTGGAG 301
QY 192 CTCTAGCGCTCTACGTTTACCTGTCATGCTTACTACTTTTGACCGCGATGATGGCT 251
DB 302 CTCTAGCGCTCTACGTTTACCTGTCATGCTTACTACTTTTGACCGCGATGATGGCT 361
QY 252 TTGAGAACTTGGCAATATCTTCTTACCAATCTCATGAGAGAGGAACTGCTGAG 311
DB 362 TTGAGAACTTGGCAATATCTTCTTACCAATCTCATGAGAGAGGAACTGCTGAG 421
QY 312 AAATGATGAAGCTGCAGAAACAAAGAGTGGCGCAATCTTCTTTCAGGATCAAGAAA 371
DB 422 AAATGATGAAGCTGCAGAAACAAAGAGTGGCGCAATCTTCTTTCAGGATCAAGAAA 481
QY 372 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTTTGAAT 431
DB 482 CCAGACTGTGATGACTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTTTGAAT 541
QY 432 AAAAATGCAATCAGTCACTACTGGAATCC 462
DB 542 AAAAATGCAATCAGTCACTACTGGAATGC 572
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ORIGIN
Query Match 42.1%; Score 374.8; DB 5; Length 1001;
Best Local Similarity 99.5%; Pred. No. 8.4e-98;
Matches 376; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 146 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGTCTAGCCTCTTA 205
DB 265 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGTCTAGCCTCTTA 324
QY 206 CGTTTACCTGCTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTC 265
DB 325 CGTTTACCTGCTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTC 384
QY 266 CAATATCTTCTTACCAATCTCATGAGAGAGGAAATGCTGAGAACTGATGAAGCT 325
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    /clone_lib="NIH MGC 112"
    /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
    EcoRI; cdna made by oligo-dt priming. Directionally cloned
    into EcoRI/XhoI sites using the following 5' adaptor:
    GGCACGAG(G). Library constructed by Ling Hong in the
    laboratory of Gerald M. Rubin (University of California,
    Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
    Superscript II RT (Life Technologies). Note: this is a
    NIH_MGC Library."
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QY 142 ACTACCAAGGACTCAGAGGCGGCATCAACCGCAGATCAACTGGAGCTCTACGCT 201
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Db 210 ACTACCAAGGACTCAGAGGCGGCATCAACCGCAGATCAACTGGAGCTCTACGCT 269
QY 202 CTTAGTTTACCTGTCCTTACTTCTTACTTTGACCGGATGATGCTTTGAAGAAGT 261
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Db 270 CTTAGTTTACCTGTCCTTACTTCTTACTTTGACCGGATGATGCTTTGAAGAAGT 329
QY 262 TTGCCAAATACCTTTCTTCAACCAATCTCATGAGGAGGAAACATCTGAGAACTGATGA 321
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Db 330 TTGCCAAATACCTTTCTTCAACCAATCTCATGAGGAGGAAACATCTGAGAACTGATGA 389
QY 332 AGCTCAGAACCAAGAGGTGCGCCAAATCTTCTTCAAGATATCAAGAAACAGACTGTG 381
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QY 382 ATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTGCTTACATTTGGAATAAATGTGA 441
    |||||
Db 450 ATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTGCTTACATTTGGAATAAATGTGA 509
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Db 510 ATCAGTCACTACTGGAATTC 530
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LOCUS BF983589 875 bp mRNA linear EST 23-JAN-2001
DEFINITION 602306579F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4398138 5',
    mRNA sequence.
ACCESSION BF983589
VERSION BF983589.1 GI:12386401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10099 row: m column: 19
High quality sequence stop: 820.
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            /clone="IMAGE:4398138"
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            /clone_lib="NIH MGC 88"
            /note="Organ: small intestine; Vector: pCMV-SPORT6;
            site 1: NotI; Site 2: SalI; Cloned unidirectionally;
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            Technologies. Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 42.0%; Score 374.6; DB 4; Length 875;
Best Local Similarity 99.0%; Pred. No. 9.2e-98;
Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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    |||||
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QY 382 ATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTGCTTACATTTGGAATAAATGTGA 441
    |||||
Db 465 ATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTGCTTACATTTGGAATAAATGTGA 524
QY 442 ATCAGTCACTACTGGAATTC 462
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Db 525 ATCAGTCACTACTGGAATTC 545
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ACCESSION BE740697
VERSION BE740697.1 GI:10154689
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM809 row: f column: 18
High quality sequence stop: 819.
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FEATURES
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            /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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source

ORIGIN

Query Match 42.0%; Score 374.6; DB 2; Length 942;
 Best Local Similarity 99.0%; Pred. No. 9.4e-98;
 Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 DB 118 CCGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 177
 |
 QY 142 ACTACACAGGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGGCTCTACGGCT 201
 |
 DB 178 ACTACACAGGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGGCTCTACGGCT 237
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 QY 202 CTTAGCTTTACTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACT 261
 |
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 DB 298 TTGCCAAATACTTTTCCACCAATCTCATGAGGAGGAGGAACTGATGA 357
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 DB 358 AGCTGCAGAACCAAGAGGTGCGCAATCTTCTTCCAGGATATCAAGAAACCGAGACTGTG 417
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 QY 382 ATGACTGGAGAGCGGGCTGAATCAATGAGTGTGCATTACATTTGGAATAAATGTGA 441
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RESULT 13
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 VERSION BF976359.1 GI:12343676
 KEYWORDS EST.
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 953)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
 Plate: LLCN1206 row: d column: 23
 High quality sequence stop: 716.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4395334"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the

FEATURES
 source

following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 42.0%; Score 374.6; DB 4; Length 953;
 Best Local Similarity 99.0%; Pred. No. 9.5e-98;
 Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 82 GAGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 141
 |
 DB 167 CCGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 226
 |
 QY 142 ACTACACAGGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGGCTCTACGGCT 201
 |
 DB 227 ACTACACAGGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGGCTCTACGGCT 286
 |
 QY 202 CTTAGCTTTACTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACT 261
 |
 DB 287 CTTAGCTTTACTGTCCATGTCTTACTACTTTTGACCGCGATGATGGCTTTGAAGAACT 346
 |
 QY 262 TTGCCAAATACTTTTCCACCAATCTCATGAGGAGGAGGAACTGATGA 321
 |
 DB 347 TTGCCAAATACTTTTCCACCAATCTCATGAGGAGGAGGAACTGATGA 406
 |
 QY 322 AGCTGCAGAACCAAGAGGTGCGCAATCTTCTTCCAGGATATCAAGAAACCGAGACTGTG 381
 |
 DB 407 AGCTGCAGAACCAAGAGGTGCGCAATCTTCTTCCAGGATATCAAGAAACCGAGACTGTG 466
 |
 QY 382 ATGACTGGAGAGCGGGCTGAATCAATGAGTGTGCATTACATTTGGAATAAATGTGA 441
 |
 DB 467 ATGACTGGAGAGCGGGCTGAATCAATGAGTGTGCATTACATTTGGAATAAATGTGA 526
 |
 QY 442 ATCACTCACTACTGGAATTC 462
 |
 DB 527 ATCACTCACTACTGGAATTC 547

RESULT 14
 BQ637251
 LOCUS 507 bp mRNA linear EST 15-JUL-2002
 DEFINITION he07f05.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
 Homo sapiens cDNA clone he07f05 5', mRNA sequence.
 ACCESSION BQ637251
 VERSION BQ637251.1 GI:21761710
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 507)
 AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
 TITLE Expressed sequence tag analysis of human retina for the NEIBank
 Project: Rebinding, an abundant, novel retinal cDNA and alternative
 splicing of other retina-preferred gene transcripts
 JOURNAL Mol. Vis. 8 (4), 196-204 (2002)
 MEDLINE 22103461
 PUBMED 12107411
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeame@helix.nih.gov
 Plate: 07 row: f column: 05
 Seq primer: M13rpl reverse primer (ABI).
 Location/Qualifiers
 1..507

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:33:36 ; Search time 176 Seconds
(without alignment)
480.074 Million cell updates/sec

Title: US-09-786-867C-5
Perfect score: 893
Sequence: 1 MTTASTQVRQNYHQDSEAA.....PRRRKRPHSIPTILIFRSP 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	890	99.7	165	Q8TD27	Q8td27 homo sapien
2	615.5	68.9	232	Q6NS36	Q6ns36 homo sapien
3	610.5	68.4	182	Q6NS36	P02794 homo sapien
4	605.5	67.8	183	Q6NZ44	Q6nz44 homo sapien
5	589.5	66.0	182	Q6NS36	Q9xt73 trichosurus
6	589.5	66.0	183	Q95MP7	Q95mp7 canis famil
7	586.5	65.7	182	Q920K4	Q920k4 cavia porce
8	585	65.5	197	Q6P9V2	Q6p9v2 rattus norv
9	583.5	65.3	220	Q66H15	Q66h15 rattus norv
10	583.5	65.3	229	Q6AYV6	Q6ayv6 rattus norv
11	580.5	65.0	185	Q6NS36	P29389 cricetus
12	575.5	64.4	181	Q6NS36	P09528 mus musculu
13	573.5	64.2	181	Q6NS36	P19132 rattus norv
14	570.5	63.9	182	Q6MIP0	Q6mip0 equus cabal
15	560.5	62.8	170	Q6NS36	P18685 ovis aries
16	560.5	62.8	179	Q6NS36	P08267 gallus gall
17	560.5	62.8	180	Q6NS36	O46414 bos taurus
18	560.5	62.8	181	Q6PRV1	Q6prv1 coturnix co
19	516.5	57.8	177	Q6NS36	O7zxm8 xenopus lae
20	515.5	57.7	177	Q6NS36	Q6zdb5 xenopus tro
21	514.5	57.6	169	Q6NS36	Q6zdb5 bos taurus
22	514.5	57.6	177	Q6NS36	P78xax6 xenopus lae
23	508.5	56.9	180	Q6NS36	P19130 sus scrofa
24	500	56.0	157	Q6NS36	P7zxt8 oreochromis
25	499.5	55.9	164	Q6NS36	P25915 oryctolagus
26	494	55.3	100	Q6NS36	Q862j4 bos taurus
27	494	55.3	242	Q6NS36	Q8n4e7 homo sapien
28	488.5	54.7	152	Q6NS36	Q6eeb2 latimeria c
29	480	53.8	132	Q6NS36	Q6y241 pagrus majo
30	479	53.6	237	Q6NS36	Q9d5f4 mus musculu
31	477	53.4	262	Q6NS36	Q9d5h4 mus musculu

32	475	53.2	177	1	FRH_SALSA	P49946 salmo salar
33	469	52.5	177	2	Q8DDT0	Q8ddt0 brachydanio
34	460.5	51.6	175	2	Q801J6	Q801j6 scyllorhinu
35	458	51.3	177	2	Q66HX7	Q66hx7 brachydanio
36	457	51.2	92	2	Q862D5	Q862d5 bos taurus
37	456.5	51.1	127	2	Q862R4	Q862r4 bos taurus
38	453	50.7	176	2	Q98TT0	Q98tt0 oncorhynch
39	441	49.4	156	2	Q8EEB1	Q8eeb1 protopteris
40	440	49.3	177	2	Q801J5	Q801j5 petromyzon
41	439	49.2	173	1	FRIS_LYMT	P42577 lymaea sta
42	436	48.8	134	2	Q86QN8	Q86qn8 branchiost
43	436	48.8	172	2	Q6WNW7	Q6wnw7 branchiost
44	435.5	48.8	149	2	Q9GMG9	Q9gmg9 macaca mula
45	435.5	48.8	174	2	Q86LZ3	Q86lz3 branchiost

ALIGNMENTS

RESULT 1
Q8TD27 PRELIMINARY; PRT; 165 AA.
ID Q8TD27
AC Q8TD27;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Placenta immunoregulatory factor PLIF.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21935397; PubMed=11821435; DOI=10.1074/jbc.M200956200;
RA Moroz C., Traub L., Maymon R., Zahalka M.A.;
RT "PLIF, a novel human ferritin subunit from placenta with
immunorepressive activity";
RL J. Biol. Chem. 277:12901-12905(2002).
CC -1- SIMILARITY: Belongs to the ferritin family.
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AY033611; AAK55486.1; -;
DR HSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0019900; F:kinase binding; NAS.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dp.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 165 AA; 19490 MW; C4849C853FCABAB6 CRC64;

Query Match 99.7%; Score 890; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.1e-71;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTTASTQVRQNYHQDSEAAINRQINLEYASYVLSMSYFDRDDVAKNFKAKYFLHQ	60
Db	1	MTTASTQVRQNYHQDSEAAINRQINLEYASYVLSMSYFDRDDVAKNFKAKYFLHQ	60
Qy	61	HEERQHAELKMLQNGRIFLODIKKPDCDDNESGLNAMECALHLEKNVNSLLEPP	120
Db	61	HEERQHAELKMLQNGRIFLODIKKPDCDDNESGLNAMECALHLEKNVNSLLEPP	120
Qy	121	PISPSPCSWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP	165
Db	121	PISPSPCSWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP	165

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RESULT 2
Q6NS36 PRELIMINARY; PRT; 232 AA.
ID AC Q6NS36;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FTH1 protein (Fragment).
GN Name=FTH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
in a soluble, nontoxic, readily available form. The functional
molecule, which is composed of 24 chains, is roughly spherical and
contains a central cavity into which the polymeric ferric iron
core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; BC070494; AAH70494.1; -.
DR HSP; P02791; 1AEW.
DR GO; GO:0005486; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; iron storage; Metal-Binding.
FT NON_TER
SQ SEQUENCE 232 AA; 26219 MW; 6C17564616345A85 CRC64;

Query Match 68.9%; Score 615.5; DB 2; Length 232;
Best Local Similarity 84.6%; Pred. No. 5.4e-47;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Chaubhwalé V.M., Dhar M., McLachlan D.R., Joshi J.G.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 [8]
 RP SEQUENCE FROM N.A.
 RA Franco A.V., Gray C.P., Myers K., Hersey P.;
 RT "Detection of ferritin heavy chain by SEREX: a multifunctional
 RT molecule in malignant tumour cells."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon adenocarcinoma;
 RA Shichijo S., Itoh K.;
 RT "Identification of immuno-peptidomics that recognized by tumor-reactive
 RT CTL generated from TIL of colon cancer patients."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [10]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Cervix, Colon, Lung, Ovary, and Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA Schnerch A., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [11]
 RP SEQUENCE OF 127-182 FROM N.A.
 RX MEDLINE=84272711; PubMed=6589621;
 RA Boyd D., Jain S.K., Crampton J., Barrett K.J., Drysdale J.;
 RT "Isolation and characterization of a cDNA clone for human ferritin
 RT heavy chain."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4751-4755(1984).
 [12]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=91125486; PubMed=1992356; DOI=10.1038/349541a0;
 RA Lawson D.M., Artymuk P.J., Yewdall S.J., Smith J.M.A.,
 RA Livingstone J.C., Treffry A., Luzzago A., Levi S., Arosio P.,
 RA Cesarini G., Thomas C.D., Shaw W.V., Harrison P.M.;
 RT "Solving the structure of human H ferritin by genetically engineering
 RT intermolecular crystal contacts."
 RL Nature 349:541-544(1991).
 [13]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97303050; PubMed=9159481; DOI=10.1006/jmbi.1997.0970;
 RA Hempstead P.D., Yewdall S.J., Fernie A.R., Lawson D.M., Artymuk P.J.,
 RA Rice D.W., Ford G.C., Harrison P.M.;
 RT "Comparison of the three-dimensional structures of recombinant human H
 RT and horse L ferritins at high resolution."
 RL J. Mol. Biol. 268:424-448(1997).
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
 CC chain and H (heavy) chain. The major chain can be light or heavy,
 CC depending on the species and tissue type.
 CC -!- SIMILARITY: In human liver the heavy chain is the major chain.
 CC -!- SIMILARITY: Belongs to the ferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 175.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M11146; AAA52437.1; -;
 DR EMBL; X03487; CAA27205.1; -;
 DR EMBL; X03488; CAA27205.1; JOINED.
 DR EMBL; X00318; CAA25086.1; ALT_FRAME.
 DR EMBL; M14212; AAA52438.1; -;
 DR EMBL; M14211; AAA52438.1; JOINED.
 DR EMBL; M12937; AAA52438.1; -;
 DR EMBL; M15383; AAA52479.1; -;
 DR EMBL; L20941; AAA35833.1; -;
 DR EMBL; AF088851; AAF89523.1; -;
 DR EMBL; AB082402; BAB93489.1; -;
 DR EMBL; BC000857; AAH00857.1; -;
 DR EMBL; BC001399; AAH01399.1; -;
 DR EMBL; BC011359; AAH11359.1; -;
 DR EMBL; BC013724; AAH13724.1; -;
 DR EMBL; BC015156; AAH15156.1; -;
 DR EMBL; BC016009; AAH16009.1; -;
 DR EMBL; BC016857; AAH16857.1; -;
 DR EMBL; BC066961; AAH66961.1; -;
 DR EMBL; M97164; AAA35832.1; -;
 DR PIR; A23517; FRHUH.
 DR PDB; 1FHA; X-ray; @=1-182.
 DR PDB; 2FHA; X-ray; @=1-182.
 DR Genew; HGNC:3976; FTH1.
 DR H-InvDB; HIX0009704; -;
 DR MIM; 134770; -;
 DR GO; GO:0008043; C:ferritin complex; TAS.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0005506; F:iron ion binding; TAS.
 DR GO; GO:0019900; F:kinase binding; ISS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0006880; P:intracellular iron ion storage; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR InterPro; IPR001519; Ferritin.
 DR InterPro; IPR009078; Ferritin/RR_like.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009040; Ferritin_Like.
 DR Pfam; PF00210; Ferritin; 1.
 DR ProDom; PD000971; Ferritin; 1.
 DR PROSITE; PS00540; FERRITIN_1; 1.
 DR PROSITE; PS00204; FERRITIN_2; 1.
 DR PROSITE; PS0905; FERRITIN_Like; 1.
 KW 3D-structure; Iron; Iron storage; Metal-binding.
 FT INIT MET 0
 FT DOMAIN 10 159 Ferritin-like diiron.
 FT METAL 27 27 Iron.
 FT METAL 58 58 Iron.
 FT METAL 61 61 Iron.
 FT METAL 62 62 Iron.
 FT METAL 64 64 Iron.
 FT METAL 65 65 Iron.
 FT METAL 107 107 Iron.
 FT METAL 141 141 Iron.
 Query Match 68.4%; Score 610.5; DB 1; Length 182;
 Best Local Similarity 84.5%; Pred No. 1.1e-46;
 Matches 120; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 2 TTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVAKNFYFLHOSH 61
 |||||
 DB 1 TTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVAKNFYFLHOSH 60
 |||||
 QY 62 EERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEFPSP 121
 |||||
 DB 61 EERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL--- 117
 |||||
 QY 122 ISPPSCWHYTTNRPPQPHL 143
 |||||
 DB 118 -----HKLATDKNDP--HL 129
 |||||

RESULT 4
 Q6NZ44 PRELIMINARY; PRT; 183 AA.
 ID Q6NZ44
 AC Q6NZ44
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan B., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited (by similarity).
 CC -!- SIMILARITY: Belongs to the ferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR EMBL; BC06341; AAH66341.1; -;
 DR HSSP; P02791; 1AEW.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001519; Ferritin.
 DR InterPro; IPR009078; Ferritin/RR like.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009040; Ferritin_like.
 DR Pfam; PF00210; Ferritin; 1.

DR ProDom; PD000971; Ferritin; 1.
 DR PROSITE; PS00540; FERRITIN_1; 1.
 DR PROSITE; PS00204; FERRITIN_2; 1.
 DR PROSITE; PS09095; FERRITIN LIKE; 1.
 KW Hypothetical protein; Iron; Iron storage; Metal-binding.
 SQ SEQUENCE 183 AA; 21441 MW; 4512B8078A2320B2 CRC64;
 |||||
 Query Match 67.8%; Score 605.5; DB 2; Length 183;
 Best Local Similarity 83.2%; Pred. No. 3.2e-46;
 Matches 119; Conservative 4; Mismatches 7; Indels 13; Gaps 2;
 |||||

QY 1 MTTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVAKNFYFLHOSH 60
 |||||
 DB 1 MTTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVAKNFYFLHOSH 60
 |||||
 QY 61 EERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
 |||||
 DB 61 EERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
 |||||
 QY 121 ISPPSCWHYTTNRPPQPHL 143
 |||||
 DB 119 -----HKLATDKNDP--HL 130
 |||||

RESULT 5
 FRIH TRIHU STANDARD; PRT; 182 AA.
 ID FRIH TRIHU
 AC Q6XT73;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ferritin heavy chain (Ferritin H subunit).
 GN Name=FTH; Synonyms=FTH;
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lactating mammary gland;
 RX MEDLINE=9227120; PubMed=10209259; DOI=10.1016/S0167-4781(99)00042-1;
 RA Demmer J., Szustak S.J., Adamski F.M., Grigor M.R.;
 RT "Cloning and expression of the transferrin and ferritin genes in a
 marsupial, the brushtail possum (Trichosurus vulpecula).";
 RL Biochim. Biophys. Acta 1445:65-74 (1999).
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited (by similarity).
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- SIMILARITY: Belongs to the ferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF092509; AAD38330.1; -;
 DR HSSP; P02794; 2FHA.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0019900; F:kinase binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR InterPro; IPR001519; Ferritin.
 DR InterPro; IPR009078; Ferritin/RR like.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009040; Ferritin_like.
 DR Pfam; PF00210; Ferritin; 1.

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DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
FT INIT MET 0 0 By similarity.
FT DOMAIN 10 159 Ferritin-like diiron.
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
SQ SEQUENCE 182 AA; 21163 MW; 22C85E4AC8C852F CRC64;

Query Match 66.0%; Score 589.5; DB 1; Length 182;
Best Local Similarity 82.4%; Pred. No. 8.5e-45;
Matches 117; Conservative 4; Mismatches 8; Indels 13; Gaps 2;

QY 2 TTASTSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 61
D 1 TTSSPSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 60
QY 62 EERQHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPSP 121
D 61 EEREHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPSP 117
QY 122 ISPPSCWHYTTNRPOQHHL 143
D 118 -----HKLATDKNDP--HL 129

RESULT 6
Q95MP7
ID Q95MP7 PRELIMINARY; PRT; 183 AA.
AC Q95MP7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeoung D., Jung H.; Kim H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
DR NCBI_TaxID=9615;
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 183 AA; 21308 MW; 9D22750A1AC4BE72 CRC64;

Query Match 65.7%; Score 586.5; DB 2; Length 182;
Best Local Similarity 81.1%; Pred. No. 1.6e-44;
Matches 116; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY 1 MTTASTSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 60
D 1 MTTASPSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 60
QY 61 HEERQHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPSP 120
D 61 HEEREHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKSNQSLLEPSP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
D 119 -----HKLATDKNDP--HL 130

RESULT 7
Q920K4
ID Q920K4 PRELIMINARY; PRT; 182 AA.
AC Q920K4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin heavy chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Hartley; TISSUE=Spleen;
RA Takagi R., Ohtani M., Watanabe N., Kobayashi Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
DR EMBL; AB073371; BAB70615.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 182 AA; 21163 MW; E5E12825DE10BE66 CRC64;

Query Match 65.7%; Score 586.5; DB 2; Length 182;
Best Local Similarity 81.1%; Pred. No. 1.6e-44;
Matches 116; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY 1 MTTASTSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 60
D 1 MTTASPSQVRNQHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHOSH 60
QY 61 HEERQHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPSP 120
D 61 HEEREHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKSNQSLLEPSP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
D 119 -----HKLATDKNDP--HL 130

RESULT 8
```


Db 157 -----HKLATDKNDP--HL 168

RESULT 10

Q6AYV6 PRELIMINARY; PRT; 229 AA.

ID Q6AYV6 AC Q6AYV6

DT 25-OCT-2004 (TREMELrel. 28, Created)

DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)

DE Fth1 protein (Fragment).

GN Name=Fth1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

EX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Skalsoda J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Grimwood U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RA Director MGC Project;

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC in a soluble, nontoxic, readily available form. The functional

CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron

CC core is deposited (By similarity).

CC -!- SIMILARITY: Belongs to the ferritin family.

CC EMBL; BC078892; AAH78892.1; -.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0008199; F:ferric iron binding; IEA.

DR GO; GO:0006879; P:iron ion homeostasis; IEA.

DR GO; GO:0006826; P:iron ion transport; IEA.

DR InterPro; IPR001519; Ferritin.

DR InterPro; IPR009078; Ferritin/RR like.

DR InterPro; IPR008331; Ferritin_Dps.

DR InterPro; IPR009040; Ferritin_like.

DR Pfam; PF00210; Ferritin; 1.

DR ProDom; PD000971; Ferritin; 1.

DR ProDom; PD000971; Ferritin; 1.

DR PROSITE; PS00540; FERRITIN_1; 1.

DR PROSITE; PS00204; FERRITIN_2; 1.

DR PROSITE; PS03050; FERRITIN_LIKE; 1.

KW Iron; iron storage; Metal-Binding.

FT NON_TER

FT SEQUENCE 229 AA; 26026 MW; BD826EA2B682D74B CRC64;

Query Match 65.3%; Score 583.5; DB 2; Length 229;

Best Local Similarity 81.8%; Pred. No. 3.8e-44;

Matches 117; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSVQVRYNHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNPKAKYFLHQ 60

DB 48 MTTASPSQVRYNHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNPKAKYFLHQ 107

QY 61 HEERQHAELKMLQNGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVQNSLLEPFS 120

DB 108 HEERHAELKMLQNGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVQNSLLEPFS 165

QY 121 PISPSPCSWHYHTNRPQPHHL 143

DB 166 -----HKLATDKNDP--HL 177

RESULT 11

FRH CRIGR STANDARD; PRT; 185 AA.

ID FRH CRIGR AC P29389;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DE Ferritin heavy chain (Ferritin H subunit).

GN Name=FRH;

OS Cricetus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Cricetulus.

OX NCBI_TaxID=10029;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=92375120; PubMed=1380656; DOI=10.1016/0921-8777(92)90069-F;

RA Zhu W., Keng P., Chou W.G.;

RT "Differential gene expression in wild-type and X-ray-sensitive mutants

RT of Chinese hamster ovary cell lines."

RL Mutat. Res. 274:237-245(1992).

CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron

CC in a soluble, nontoxic, readily available form. The functional

CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron

CC core is deposited.

CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)

CC chain and H (heavy) chain. The major chain can be light or heavy,

CC depending on the species and tissue type.

CC -!- SIMILARITY: Belongs to the ferritin family.

CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M99692; AAB46388.1; -.

DR HSSP; P02794; 2FHA.

DR GO; GO:0005886; C:plasma membrane; ISS.

DR GO; GO:0019900; F:kinase binding; ISS.

DR GO; GO:0006955; P:immune response; ISS.

DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.

DR InterPro; IPR001519; Ferritin.

DR InterPro; IPR009078; Ferritin/RR like.

DR InterPro; IPR008331; Ferritin_Dps.

DR InterPro; IPR009040; Ferritin_like.

DR Pfam; PF00210; Ferritin; 1.

DR ProDom; PD000971; Ferritin; 1.

DR PROSITE; PS00540; FERRITIN_1; 1.

DR PROSITE; PS00204; FERRITIN_2; 1.

DR PROSITE; PS03050; FERRITIN_LIKE; 1.

KW Iron; iron storage; Metal-Binding.

FT INIT_MET 0 By similarity.

FT DOMAIN 15 164 Ferritin-like diiron.

FT METAL 32 32 Iron (By similarity).

```
FT METAL 63 Iron (By similarity).
FT METAL 66 Iron (By similarity).
FT METAL 67 Iron (By similarity).
FT METAL 69 Iron (By similarity).
FT METAL 70 Iron (By similarity).
FT METAL 112 Iron (By similarity).
FT METAL 146 Iron (By similarity).
SQ SEQUENCE 185 AA; 21355 MW; E665373DF43C82C4 CRC64;

Query Match 65.0%; Score 580.5; DB 1; Length 185;
Best Local Similarity 81.1%; Pred.No. 5.5e-44;
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSVQRVYHODSEAINRQINLELYASYVYLSMYSYFDRDDVALKNFYKVFHQH 60
DB 5 LTTASPSQVRVYHODSEAINRQINLELYASYVYLSMYSYFDRDDVALKNFYKVFHQH 64

QY 61 HEERQHAELKMLQNGRGRIFLDQIKPKDCDDWESGLNAMECALHLEKYNQSLLEPPS 120
DB 65 HEERQHAELKMLQNGRGRIFLDQIKPKDCDDWESGLNAMECALHLEKYNQSLLEPPS 122

QY 121 PISPSPCWYHYYTNRPOQHLL 143
DB 123 -----HKLATDKNDP--HL 134

RESULT 12
FRIH_MOUSE STANDARD; PRT; 181 AA.
AC P09528;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
GN Name=Fth;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RX MEDLINE=90016900; PubMed=2798146;
RA Yachau A., Renaudie F., Grandchamp B., Beaumont C.;
RT "Nucleotide sequence of the mouse ferritin H chain gene.";
RL Nucleic Acids Res. 17:8005-8005(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=89057487; PubMed=3194211;
RA Miyazaki Y., Setoguchi M., Higuchi Y., Yoshida S., Akizuki S.,
RA Yamamoto S.;
RT "Nucleotide sequence of cDNA encoding the heavy subunit of mouse
RT macrophage ferritin.";
RL Nucleic Acids Res. 16:10373-10373(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315064; PubMed=3410854;
RA Torti S.V., Kwak E.L., Miller S.C., Miller L.L., Ringold G.M.,
RA Myambo K.B., Young A.P., Torti F.M.;
RT "The molecular cloning and characterization of murine ferritin heavy
RT chain, a tumor necrosis factor-inducible gene.";
RL J. Biol. Chem. 263:12638-12644(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078648; PubMed=2258056; DOI=10.1016/0378-1119(90)90396-9;
RA Kwak E.L., Torti S.V., Torti F.M.;
RT "Murine ferritin heavy chain: isolation and characterization of a
RT functional gene.";
RL Gene 94:255-261(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214195; PubMed=2708374;
```

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RA Beaumont C., Dugast I., Renaudie F., Souroujon M., Grandchamp B.;
RT "Transcriptional regulation of ferritin H and L subunits in adult
RT erythroid and liver cells from the mouse. Unambiguous identification
RT of mouse ferritin subunits and in vitro formation of the ferritin
RT shells.";
RL J. Biol. Chem. 264:7498-7504(1989).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaldo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriell L.M., Kaplan A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Negashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078648; PubMed=2258056; DOI=10.1016/0378-1119(90)90396-9;
RA Kwak E.L., Torti S.V., Torti F.M.;
RT "Murine ferritin heavy chain: isolation and characterization of a
RT functional gene.";
RL Gene 94:255-261(1990).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214195; PubMed=2708374;
```

-!- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited.

-!- MISCELLANEOUS: There are two types of ferritin subunits: L (light) chain and H (heavy) chain. The major chain can be light or heavy, depending on the species and tissue type.

-!- SIMILARITY: Belongs to the ferritin family.

-!- SIMILARITY: Contains 1 ferritin-like diiron domain.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X52561; CAA3795.1; -
 DR EMBL; X12812; CAA31300.1; -
 DR EMBL; J03941; AAA37611.1; -
 DR EMBL; M60170; AAA37613.1; -
 DR EMBL; M24509; AAA37612.1; -
 DR EMBL; AK027998; BAC25694.1; -
 DR EMBL; BC012314; AAA2314.1; -
 DR PIR; S06070; S06070.
 DR HSSP; P02794; 2FHA.
 DR MGD; MGI:95588; Fth.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0019900; P:kinase binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR InterPro; IPR001519; Ferritin.
 DR InterPro; IPR009078; Ferritin/RR like.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009040; Ferritin_like.
 DR Pfam; PF00210; Ferritin; 1.
 DR ProDom; PD000971; Ferritin; 1.
 DR PROSITE; PS00540; FERRITIN_1; 1.
 DR PROSITE; PS00204; FERRITIN_2; 1.
 DR PROSITE; PS00905; FERRITIN_LIKE; 1.
 KW Iron; Iron storage; Metal-binding.
 FT INIT MET 0
 FT DOMAIN 10 159 Ferritin-like diiron.
 FT METAL 27 27 Iron (By similarity).
 FT METAL 61 61 Iron (By similarity).
 FT METAL 62 62 Iron (By similarity).
 FT METAL 65 65 Iron (By similarity).
 FT METAL 107 107 Iron (By similarity).
 FT METAL 141 141 Iron (By similarity).
 FT CONFLICT 16 16 A -> S (in Ref. 5).
 FT CONFLICT 136 136 Y -> H (in Ref. 5).
 FT CONFLICT 139 139 S -> N (in Ref. 5).
 FT CONFLICT 163 163 A -> S (in Ref. 5).
 SQ SEQUENCE 181 AA; 20935 MW; E4413587BF83889 CRC64;
 Query Match 64.4%; Score 575.5; DB 1; Length 181;
 Best Local Similarity 81.0%; Pred. No. 1.5e-43;
 Matches 115; Conservative 5; Mismatches 9; Indels 13; Gaps 2;
 Qy 2 TTASTSQVQRYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFKYFLHQSH 61
 Db 1 TTASPSQVQRYHQDAEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFKYFLHQSH 60
 Qy 62 EERQHAELKMLQNGRGRIFLDIKKDPDDESGINAMECALHLEKNVQSLLEFPSP 121
 Db 61 EERHAELKMLQNGRGRIFLDIKKDPDDESGINAMECALHLEKNVQSLLEL--- 117
 Qy 122 ISPSPCWHYHTNRQPQPHL 143
 Db 118 -----HKLATKNDP--HL 129
 RESULT 13
 ID -FRIH RAT STANDARD; PRT; 181 AA.
 AC P19132;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ferritin heavy chain (ferritin H subunit).
 GN Name=Fth;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041121; PubMed=3478702;
 RA Murray M.T., White K., Munro H.N.;
 RT "Conservation of ferritin heavy subunit gene structure: implications
 RT for the regulation of ferritin gene expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7438-7442(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Wu C.G., Groenink M., Bosma A., Reitsma P.H., van Deventer J.H.,
 RA Chamuleau R.A.F.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 136-181 FROM N.A.
 RX MEDLINE=88106597; PubMed=2827671;
 RA Ursini M.V., de Franciscis V.;
 RT "TSH regulation of ferritin H chain messenger RNA levels in the rat
 RT thyroids.";
 RL Biochem. Biophys. Res. Commun. 150:287-295(1988).
 RN [4]
 RP SEQUENCE OF 158-181.
 RC TISSUE=Liver;
 RX MEDLINE=84162134; PubMed=6546756;
 RA Leibold E.A., Aziz N., Brown A.J.P., Munro H.N.;
 RT "Conservation in rat liver of light and heavy subunit sequences of
 RT mammalian ferritin. Presence of unique octopeptide in the light
 RT subunit.";
 RL J. Biol. Chem. 259:4327-4334(1984).
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 CC in a soluble, nontoxic, readily available form. The functional
 CC molecule, which is composed of 24 chains, is roughly spherical and
 CC contains a central cavity into which the polymeric ferric iron
 CC core is deposited.
 CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
 CC chain and H (heavy) chain. The major chain can be light or heavy,
 CC depending on the species and tissue type.
 CC -!- SIMILARITY: Belongs to the ferritin family.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 CC -----
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 CC -----
 DR EMBL; M18053; AAA41153.1; -
 DR EMBL; M18051; AAA41153.1; JOINED.
 DR EMBL; M18052; AAA41153.1; JOINED.
 DR EMBL; U58829; AAB39690.1; -
 DR EMBL; M29330; AAA42300.1; -
 DR PIR; A39884; A39884.
 DR HSSP; P02794; 2FHA.
 DR GO; GO:0005886; C:plasma membrane; ISS.
 DR GO; GO:0019900; P:kinase binding; ISS.
 DR GO; GO:0006955; P:immune response; ISS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR InterPro; IPR001519; Ferritin.
 DR InterPro; IPR009078; Ferritin/RR like.
 DR InterPro; IPR008331; Ferritin_Dps.
 DR InterPro; IPR009040; Ferritin_like.
 DR Pfam; PF00210; Ferritin; 1.
 DR ProDom; PD000971; Ferritin; 1.
 DR PROSITE; PS00540; FERRITIN_1; 1.
 DR PROSITE; PS00204; FERRITIN_2; 1.
 DR PROSITE; PS00905; FERRITIN_LIKE; 1.
 KW Direct protein sequencing; Iron; Iron storage; Metal-binding.

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FT INIT MET 0 0 Ferritin-like diiron.
FT DOMAIN 10 159 Iron (By similarity).
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
FT METAL 181 181 R -> E (in Ref. 2).
FT CONFLICT 101 101 S -> E (in Ref. 4).
SQ SEQUENCE 181 AA; 20995 MW; 0A5AD533E1706C1 CRC64;

Query Match 64.2%; Score 573.5; DB 1; Length 181;
Best Local Similarity 81.0%; Pred. No. 2.3e-43;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

QY 2 TTASTSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 61
Db |||||
QY 1 TTAFSPQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
Db |||||
QY 62 EEROHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSP 121
Db |||||
QY 61 EEREHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEL--- 117
Db |||||
QY 122 ISPSPSCWHYHTNRPQPHL 143
Db |||||
QY 118 -----HKLATDKNDP--HL 129
Db |||||

RESULT 14
QMIPO PRELIMINARY; PRT; 182 AA.
AC Q8MIPO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin heavy chain.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; AY12742; XAM51631.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin/RR like.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN LIKE; 1.
KW Iron; Iron storage; Metal-binding.
SQ SEQUENCE 182 AA; 21269 MW; 2282186D630F1A0D CRC64;

Query Match 63.9%; Score 570.5; DB 2; Length 182;
Best Local Similarity 79.0%; Pred. No. 4.2e-43;
Matches 113; Conservative 7; Mismatches 10; Indels 13; Gaps 2;
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QY 1 MTTASTSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
Db |||||
QY 1 MTTAFSPQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
Db |||||
QY 61 HEEROHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSP 120
Db |||||
QY 61 HEEREHAELKMLQNGRGRIFLQDIKKPDCDDWENGLKAMECALHLEKNVNSLLEL-- 118
Db |||||
QY 121 ISPSPSCWHYHTNRPQPHL 143
Db |||||
QY 119 -----HKLATDKNDP--HL 130
Db |||||

RESULT 15
FRIH SHEEP STANDARD; PRT; 170 AA.
AC P18685;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
CN Name=ETH;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97073147; PubMed=8915895;
RX DOI=10.1002/(SICI)1097-4547(19961015)46:2<187::AID-JNR6>3.3.CO;2-J;
RA Sanyal B., Polak P.E., Szuchet S.;
RT "Differential expression of the heavy-chain ferritin gene in non-
RT adhered and adhered oligodendrocytes.";
RL J. Neurosci. Res. 46:187-197(1996).
RN [2]
RP SEQUENCE OF 71-101.
RX MEDLINE=9286137; PubMed=2472118;
RX McKenzie R.A., Yablonski M.J., Gillespie G.Y., Theil E.C.;
RT "Crosslinks between intramolecular pairs of ferritin subunits: effects
RT on both H and L subunits and on immunoreactivity of sheep spleen
RT ferritin.";
RL Arch. Biochem. Biophys. 272:88-96(1989).
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited.
CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
CC chain and H (heavy) chain. The major chain can be light or heavy,
CC depending on the species and tissue type.
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
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CC -----
CC EMBL; U54800; AAB19186.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin like.
```

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DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR PRODOM; PRO00971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; FALSE_NEG.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Direct protein sequencing; Iron; Iron storage; Metal-binding.
FT INIT MET 0 0 By similarity.
FT DOMAIN 10 159 Ferritin-like diiron.
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
FT CONFLICT 78 78 A -> G (in Ref. 2).
SQ SEQUENCE 170 AA; 19931 MW; 32FD337E11F16FD0 CRC64;

Query Match 62.8%; Score 560.5; DB 1; Length 170;
Best Local Similarity 78.9%; Pred. No. 3.1e-42;
Matches 112; Conservative 6; Mismatches 11; Indels 13; Gaps 2;

Qy 2 TTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQSH 61
Db 1 TTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQSH 60

Qy 62 EERQHAELMKLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSP 121
Db 61 EEREHAERLMKLQNGRGRIFLQDIKKPDRDDWENGLNAMECALCLERSVNSQLLEL--- 117

Qy 122 ISPSFSCWHYTTNRPQPHL 143
Db 118 -----HKLATEKNDP--HL 129
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Search completed: March 30, 2005, 19:42:13
Job time : 182 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:30:30 ; Search time 72 Seconds
(without alignments)
886.326 Million cell updates/sec

Title: US-09-786-867C-5
Perfect score: 893
Sequence: 1 MTTASTSQVRQYHODSEAA.....PARRKRPHSIPTPIIFRSP 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	881	98.7	165	3	AAY53271 Human onc
2	615.5	68.9	183	2	AAR71567 Human mon
3	615.5	68.9	183	4	AAB90804 Human she
4	615.5	68.9	183	7	ADD22444 HLA-B46 T
5	615.5	68.9	183	7	AD115887 Human pp
6	615.5	68.9	183	8	ABM81295 Tumour-as
7	615.5	68.9	190	7	ADG42360 Ferritin
8	615.5	68.9	190	8	ADG29701 Human col
9	615.5	68.9	190	8	ADP24691 PRO polyyp
10	615.5	68.9	206	5	ABB97273 Novel hum
11	615.5	68.9	222	6	ABR41768 Human DIT
12	615.5	68.9	362	8	ADG82746 Recombina
13	610.5	68.4	183	7	ADN31067 Human H-c
14	580.5	65.0	180	5	ABP69305 Human pol
15	580.5	65.0	182	4	AAU27741 Mouse fol
16	580.5	65.0	227	6	ABU11456 Human MDD
17	579	64.8	165	8	ABM81021 Tumour-as
18	540	60.5	148	4	AAO04400 Human pol
19	523.5	58.6	127	5	ABP42274 Human ova
20	494	55.3	242	5	ABG32428 Human sec
21	477	53.4	173	4	AAE09630 Human gen
22	477	53.4	173	7	ADG62935 Novel hum
23	424.5	47.5	146	8	ABM80602 Tumour-as
24	421.5	47.2	273	8	ABM80723 Tumour-as
25	421	47.1	621	4	ABG28304 Novel hum

26	416.5	46.6	275	4	ABG21478	Novel hum
27	399	44.7	183	4	AAU07890	Polypepti
28	399	44.7	183	7	ADG84955	Cancer-as
29	399	44.7	713	4	ABG12069	Novel hum
30	399	44.7	713	4	ABG07849	Novel hum
31	395.5	44.3	144	8	ADO43747	Amino aci
32	392	43.9	183	6	ABR82317	Human met
33	392	43.9	201	4	ABG27400	Novel hum
34	390.5	43.7	183	5	ABU65170	Human NOV
35	390.5	43.7	183	8	ADN61991	Human nov
36	390.5	43.7	317	7	ADC31487	Human nov
37	387.5	43.4	204	6	ABB99663	Amino aci
38	379.5	42.5	178	8	ABO59224	Human gen
39	379	42.4	248	4	ABG27399	Novel hum
40	377	42.2	141	4	ABG17463	Novel hum
41	375.5	42.0	221	4	AAU07889	Polypepti
42	361	40.4	85	3	AAE58474	Lung canc
43	343	38.4	199	5	ABP51378	Human MDD
44	324.5	36.3	153	6	ABU70932	Human adi
45	316	35.4	175	6	ABR64209	Angiogene

ALIGNMENTS

RESULT 1
AAY53271
ID AAY53271 standard; protein; 165 AA.

XX AC AAY53271;
XX DT 20-JUL-2000 (first entry)
XX DE Human oncofoetal ferritin 1 protein sequence.
XX KW Human; oncofoetal ferritin 1; OFF1; ferritin; transplation;
KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;
KW contraceptive; abortive; nontropic; vaccine; immunisation; cancer;
KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;
KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;
KW spontaneous abortion; miscarriage; premature contraction; toxemia;
KW premature delivery.

XX OS Homo sapiens.

XX PN WO200015788-A2.

XX PD 23-MAR-2000.

XX XX 08-SEP-1999; 99WO-IL000485.

XX XX 11-SEP-1998; 98IL-00126181.

XX PA (GARD-) GARDINO INVESTMENT NV.

XX XX Moroz C;

XX WPI; 2000-271427/23.

XX N-PSDB; AAA13647.

XX PT DNA sequence coding for oncofetal ferritin 1 protein, useful for
PT immunisations against breast cancer, for enhancing fertilization rates
PT during in vitro fertilization treatment and for use as a growth factor of
PT bone-marrow progenitor cells.

XX PS Example 7; Fig 5; 60pp; English.

XX CC The present sequence represents the human oncofetal ferritin 1 (OFF1)
CC protein. OFF1 has cytostatic, immunosuppressive, contraceptive, abortive
CC and nontropic activities, and can be used as a vaccine. Compositions
CC comprising the expression vector containing an OFF1 coding sequence, and
CC the OFF1 protein, are useful: (a) for immunisations against cancer,

CC especially breast cancer; (b) in the treatment of transplant rejections,
 CC autoimmune diseases, pathological pregnancies; (c) for enhancing
 CC fertilisation rates during in vitro fertilisation (IVF) treatment; and
 CC (d) for use as a growth factor of bone-marrow progenitor cells such as
 CC granulocyte monocytes. The OFF1 nucleotide sequence is useful for
 CC diagnosing cancer such as breast cancer, hepatoblastoma, leukaemia,
 CC Hodgkin's and non-Hodgkin's lymphomas and embryonal tumours, Down's
 CC Syndrome, and pathological pregnancies such as spontaneous abortion and
 CC miscarriage, premature contractions, toxemia or premature delivery
 XX Sequence 165 AA;

Query Match 98.7%; Score 881; DB 3; Length 165;
 Best Local Similarity 98.8%; Pred. No. 6.4e-90;
 Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60
 Db |||||
 QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60
 Db |||||
 QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
 Db |||||
 QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
 Db |||||
 QY 121 PISPSPCSWHHYTTNRPOQHLLRPRRKRPHSIPTPIIFRSP 165
 Db |||||
 QY 121 PISPSPCSWHHYTTNRPEQHLLRPRRKRPHSIPTPIIFRSP 165
 Db |||||

RESULT 2

AAR71567

ID AAR71567 standard; protein; 183 AA.

XX

AC AAR71567;

XX 01-NOV-1995 (first entry)

XX Human monocyte growth factor.

XX Monocyte growth factor; human; lung; cancer cell line;
 KW cellular immune function; macrophage.
 XX Homo sapiens.

XX JP07031482-A.

XX 03-FEB-1995.

XX 21-JUL-1993; 93JP-00200129.

XX 21-JUL-1993; 93JP-00200129.

XX (LIPE-) ZH LIFE TECHNOLOGY KENKYUSHO.

XX WPI: 1995-109536/15.

XX N-PSDB; AAQ85979.

XX Recombinant human monocyte growth factor and its coding DNA - useful for
 XX stimulation of cellular immune function and macrophage.
 XX Claim 1; Page 2; 12pp; Japanese.

XX The amino acid sequence of a novel monocyte growth factor. The protein
 XX was isolated from a human lung cancer cell line, T3M-30Lu (FERM BP1120).
 XX The sequence of the protein was determined by amino acid sequencing
 XX following cleavage of the purified protein by V8 protease. The gene
 XX encoding this protein can be used to produce recombinant monocyte growth
 XX factor which can be used for stimulation of cellular immune function and
 XX macrophages

XX Sequence 183 AA;

Query Match 68.9%; Score 615.5; DB 2; Length 183;
 Best Local Similarity 84.6%; Pred. No. 3.7e-60;
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

Best Local Similarity 84.6%; Pred. No. 3.7e-60;
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
 QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60
 Db |||||
 QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60
 Db |||||
 QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
 Db |||||
 QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
 Db |||||
 QY 121 PISPSPCSWHHYTTNRPOQHLL 143
 Db |||||
 QY 119 -----HKLATDKNDP--HL 130
 Db |||||

RESULT 3

AAB90804

ID AAB90804 standard; protein; 183 AA.

XX

AC AAB90804;

XX 15-JUN-2001 (first entry)

XX Human shear stress-response protein SEQ ID NO: 108.

XX Human; shear stress-response protein; vascular disease; arteriosclerosis.
 XX Homo sapiens.

XX WO200125427-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-JP006840.

XX 01-OCT-1999; 99JP-00280976.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (NOJI/) NOJIMA H.

XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;

XX Kuga T, Sekine S, Nakamura Y, Sugano S;

XX WPI: 2001-266308/27.

XX N-PSDB; AAH02927.

XX DNA sequences, proteins encoded by them and antibodies against them

XX useful in diagnosis and treatment of vascular disease caused by

XX arteriosclerosis.

XX Claim 60; Page 539-540; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a
 XX number of human shear stress response proteins. These are useful in the
 XX diagnosis, treatment and screening of vascular diseases caused by
 XX arteriosclerosis, including heart failure, post-PTCA restenosis and
 XX hypertension

XX Sequence 183 AA;

Query Match 68.9%; Score 615.5; DB 4; Length 183;

Best Local Similarity 84.6%; Pred. No. 3.7e-60;

Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60

Db |||||

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60

Db |||||

QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120

Db |||||

QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120

Db |||||


```
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 4
ADD22444
ID ADD22444 standard; protein; 183 AA.
XX
AC ADD22444;
XX
DT 15-JAN-2004 (first entry)
XX
DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 94.
XX
KW tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
KW colon; mouth; lung; prostatic; gynecological; human.
XX
OS Homo sapiens.
XX
PN JP2003111595-A.
XX
PD 15-APR-2003.
XX
PF 24-JUN-2002; 2002JP-00183603.
XX
PR 25-JUN-2001; 2001JP-00191974.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-611129/58.
XX
PT Novel tumor antigenic peptide or polypeptide useful for inducing
PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
PT prostatic or gynecological cancer.
XX
PS Claim 2; SEQ ID NO 94; 98pp; Japanese.
XX
CC The invention relates to a novel tumour antigenic peptide or polypeptide
CC comprising a sequence selected from 99 sequences fully defined in the
CC specification. The tumour antigenic peptide or polypeptide comprises a
CC sequence selected from 99 sequences fully defined in the specification,
CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
CC Pro-Leu-Sar-Gln-Glu-Thr-Phe, and the polypeptide preferably has a
CC sequence comprising 393 amino acids fully defined in the specification.
CC The invention further provides a cancer vaccine comprising a tumour
CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
CC hybridising polynucleotide, a recombinant vector containing the
CC polynucleotide, a host transformed with the vector or an antibody are
CC useful for screening for compounds that interact with the tumour
CC antigenic peptide, the polypeptide or its encoding polynucleotide and
CC increases the expression of the tumour antigenic peptide, the polypeptide
CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
CC vaccine is useful for treating cancer such as colon, mouth, lung,
CC prostatic or gynecological cancer. The invention also provides a
CC pharmaceutical composition useful for treating cancer. The tumour
CC antigenic peptide or the polypeptide is useful as an antigen to create
CC antibodies. This sequence represents one of the tumour antigenic
CC polypeptides of the invention.
XX
SQ Sequence 183 AA;
Query Match 68.9%; Score 615.5; DB 7; Length 183;
Best Local Similarity 84.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKFLHQS 60
Db 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKFLHQS 60
QY 61 HEERHAEKLMKLNQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
Db 61 HEERHAEKLMKLNQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 5
AD115887
ID AD115887 standard; protein; 183 AA.
XX
AC AD115887;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PP 84.
XX
KW tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;
KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;
KW stomach cancer; buccal cancer; renal cancer; lung cancer;
KW gynecological cancer; prostate cancer.
XX
OS Homo sapiens.
XX
PN WO2003008450-A1.
XX
PD 30-JAN-2003.
XX
PF 11-JUN-2002; 2002WO-JP005799.
XX
PR 12-JUN-2001; 2001JP-00177058.
XX
PR 21-AUG-2001; 2001JP-00250728.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Shichijo S;
XX
DR WPI; 2003-267996/26.
XX
DR N-PSDB; AD115962.
XX
PT Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or
PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of
PT cancer including preparation of cancer vaccines.
XX
PS Claim 2; SEQ ID NO 231; 323pp; Japanese.
XX
CC The invention relates to a tumour antigen peptide recognised by human
CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)
CC and/or capable of inducing CTL. The tumour antigen peptide is useful for
CC the treatment, prevention, diagnosis and vaccine production for cancers
CC including colorectal, stomach, buccal, renal, lung, gynecological and
CC prostate cancer. The present sequence represents the amino acid sequence
CC of a human protein.
XX
SQ Sequence 183 AA;
Query Match 68.9%; Score 615.5; DB 7; Length 183;
Best Local Similarity 84.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKFLHQS 60
Db 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKFLHQS 60
QY 61 HEERHAEKLMKLNQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 120
Db 61 HEERHAEKLMKLNQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130
```

RESULT 6
ABM81295
ID ABM81295 standard; protein; 183 AA.
XX
AC ABM81295;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO82035, SEQ.3340.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN39288.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3340; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 183 AA;
Query Match 68.9%; Score 615.5; DB 8; Length 183;
Best Local Similarity 84.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSVQRNQHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFYFLHQS 60
DB 1 MTTASTSVQRNQHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFYFLHQS 60

QY 61 HEERHAEKLMKLNQGRGRIFLODIKKPDCDDWESGLNAMECALHLEKKNVNSLLEPPS 120
DB 61 HEERHAEKLMKLNQGRGRIFLODIKKPDCDDWESGLNAMECALHLEKKNVNSLLEPPS 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
DB 119 -----HKLATDKNDP--HL 130
RESULT 7
ADG42360
ID ADG42360 standard; peptide; 190 AA.
XX
AC ADG42360;
XX
DT 26-FEB-2004 (first entry)
XX
DE Ferritin H chain for fusion protein construction.
XX
KW anti-HIV; virucide; vaccine; gene therapy; ferritin; fusion protein;
KW polymeric assembly; AIDS; SARS; oxygen transport; blood substitute;
KW image contrast agent; metal chelating agent; gelling agents;
KW protein purification platform.
XX
OS Homo sapiens.
XX
PN WO2003094849-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-US014617.
XX
PR 10-MAY-2002; 2002US-0379145P.
XX
PA (NEWC-) NEW CENTURY PHARM INC.
XX
PI Carter DC, Li CQ;
XX
DR WPI; 2003-903936/82.
XX
XX New ferritin fusion proteins in which ferritin is fused with a protein.
PT capable of being fused to ferritin without interfering with polymeric
PT assembly of resulting fusion protein, useful as human or veterinary
PT vaccines and therapeutics.
XX
PS Disclosure; SEQ ID NO 8; 52pp; English.
XX
XX The invention relates to a ferritin fusion protein comprising a fusion
CC protein selected from a ferritin protein fused at the C-terminus or at
CC the N-terminus with a protein or peptide capable of being fused to
CC ferritin without interfering with the polymeric assembly of the resulting
CC fusion protein. The fusion proteins are useful in the development of
CC human and veterinary vaccines and therapeutics against e.g. AIDS or SARS,
CC or in other applications including oxygen transport and the therapeutic
CC delivery of drugs and other therapeutic agents, or as blood substitutes,
CC image contrast agents, metal chelating agents, gelling agents, protein
CC purification platforms, and therapeutic receptor-binding proteins. In
CC examples of the invention, the ferritin H chain is fused to a number of
CC proteins via Gly spacer. This sequence represents the ferritin H chain
CC which is fused to a number of peptides/proteins.
XX
SQ Sequence 190 AA;
Query Match 68.9%; Score 615.5; DB 7; Length 190;
Best Local Similarity 84.6%; Pred. No. 3.9e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSVQRNQHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFYFLHQS 60
DB 1 MTTASTSVQRNQHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFYFLHQS 60
QY 61 HEERHAEKLMKLNQGRGRIFLODIKKPDCDDWESGLNAMECALHLEKKNVNSLLEPPS 120

Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNVHDSAAINRQINLELYASVYLSMSYFDRDDVALKNFAKYFLHQS 60
DB 1 MTTASTSQVRQNVHDSAAINRQINLELYASVYLSMSYFDRDDVALKNFAKYFLHQS 60

QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
DB 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120

QY 121 PISPSPCSWHHYTTNRPOQHLL 143
DB 119 -----HKLATDKNDP--HL 130

RESULT 10
ABB97273
ID ABB97273 standard; protein; 206 AA.
XX
AC ABB97273;
XX
DT 27-JUN-2002 (first entry)
XX
DE Novel human protein SEQ ID NO: 541.
XX
KW Human; antianemic; vulnary; antiinflammatory; immunomodulator;
KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR N-PSDB; ABN32459.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Example 2; SEQ ID NO 541; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a protein of the invention
XX
SQ Sequence 206 AA;

Query Match 68.9%; Score 615.5; DB 5; Length 206;
Best Local Similarity 84.6%; Pred. No. 4.3e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNVHDSAAINRQINLELYASVYLSMSYFDRDDVALKNFAKYFLHQS 60
DB 24 MTTASTSQVRQNVHDSAAINRQINLELYASVYLSMSYFDRDDVALKNFAKYFLHQS 83

QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
DB 84 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 141

QY 121 PISPSPCSWHHYTTNRPOQHLL 143
DB 142 -----HKLATDKNDP--HL 153

RESULT 11
ABR41768
ID ABR41768 standard; protein; 222 AA.
XX
AC ABR41768;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human DITHP biochemical pathway protein.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW biochemical pathway.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 19-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-129518/12.
DR N-PSDB; ACC46705.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
PS Claim 27; SEQ ID NO 1303; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening

CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which is involved in a
CC biochemical pathway. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 222 AA;

Query Match 68.9%; Score 615.5; DB 6; Length 222;
Best Local Similarity 84.6%; Pred. No. 4.8e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSVQRNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
DB 28 MTTASTSVQRNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 87
QY 61 HEERQHAELKMLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 120
DB 88 HEERHAELKMLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 145
QY 121 PISPSPCWHYTTNRPOQHLL 143
DB 146 -----HKLATDKNDP--HL 157

RESULT 12
ADQ82746
ID ADQ82746 standard; protein; 362 AA.
XX
AC ADQ82746;
XX
DT 09-SEP-2004 (first entry)
XX
DE Recombinant human ferritin protein.
XX
KW human; ferritin protein.
XX
OS Homo sapiens.
XX
PN KR2004007892-A.
XX
XX 28-JAN-2004.
XX
PF 11-JUL-2002; 2002KR-00040497.
XX
PR 11-JUL-2002; 2002KR-00040497.
XX
PA (BIOP-) BIOPROGEN CO LTD.
XX
PI Ham MS, Jung BH, Kim SU, Lee EG, Lee JW;
XX
XX WPI; 2004-386312/36.
DR N-PSDB; ADQ82747.
XX
PT New recombinant human ferritin proteins and production method of them.
XX
PS Claim 8; SEQ ID NO 11; 27pp; Korean.

CC The invention comprises the amino acid and coding sequences of a
CC recombinant human ferritin protein, the invention also comprises a
CC production method for the recombinant human ferritin protein. The present
CC amino acid sequence represents the recombinant human ferritin protein of
CC the invention.
XX
SQ Sequence 362 AA;

Query Match 68.9%; Score 615.5; DB 8; Length 362;
Best Local Similarity 84.6%; Pred. No. 9.5e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTSVQRNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
DB 1 MTTASTSVQRNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 120
DB 61 HEERHAELKMLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 118
QY 121 PISPSPCWHYTTNRPOQHLL 143
DB 119 -----HKLATDKNDP--HL 130

RESULT 13
ADN31067
ID ADN31067 standard; protein; 183 AA.
XX
AC ADN31067;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human H-chain ferritin (rHN) protein.
XX
KW human; H-chain ferritin; rHN; anaemia; iron.
XX
OS Homo sapiens.
XX
PN KR2002090036-A.
XX
PD 30-NOV-2002.
XX
PF 25-MAY-2001; 2001KR-00029187.
XX
PR 25-MAY-2001; 2001KR-00029187.
XX
PA (JUNG/) JUNG J M.
XX
PI Jung JM, Lee YJ;
XX
DR WPI; 2003-339039/32.
DR N-PSDB; ADN31064.
XX
PT Overexpression method of recombinant human h-chain ferritin in Pichia
PT pastoris and therapeutic composition for anemia using the same.
XX
PS Disclosure; Page 11; 13pp; Korean.
XX
XX This invention relates to the novel overexpression production of
CC recombinant human H-chain ferritin (rHN) in Pichia pastoris (P.
CC pastoris). Specifically, it refers to the development of pharmaceutical
CC compositions for the treatment of anaemia, due to the excellent capacity
CC of this protein for storing iron. The present invention describes
CC recombinant Pichia pastoris obtained by transformation using an
CC expression vector pGAPZ alpha A/rHN derived from Pichia pastoris and
CC containing human H-chain ferritin (rHN) gene. The human recombinant rHN
CC is a homopolymer consisting of 24 H-chains having 24000 Da and its
CC molecular weight is 576000 Da. This polypeptide sequence is the human H-
CC chain ferritin protein of the invention.
XX
SQ Sequence 183 AA;

CC platelet or coagulation disorders; wound, burns, incision, ulcers, liver
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
arthritis, etc. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 180 AA;

Query Match 65.0%; Score 580.5; DB 5; Length 180;
Best Local Similarity 81.1%; Pred.No. 2.9e-56;
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2

QY 1 MTASTSVQRVNYHQDSEAAINRINLELYASYVIYSMSYYFDRDDVALKNFAKYFLHOS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MTASPSPVRNRYHQDAEAIRINLELYASVIVLSMCSYCFPRDDVALKNFAKYFLHOS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 HEERHAELMKLQNORGGRIFFLODIKKPCDDWESGLNAMECALHLKXNVQSLLFEPS 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 HEEREHAELMKLQNORGGRIFFLDIKKPDRDDWESGLNAMECALHLEKSVMQSILLEL-- 118
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 PISPFSCWHHYTNRPPQHLL 143
|| ||:: || ||
Db 119 -----HKLATDKNDP--HL 130

RESULT 15
AAU27741

ID AAU27741 standard; protein; 182 AA.

XX AC AAU27741;
DT XX
TX XX
DE Mouse full-length polypeptide sequence #66.
XX XX
KW Mammal; human; thesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cystostatic; antiarthritic; antirheumatic; vasodilator; immunosuppressive; vasotrophic; antiparkinsonian;
KW antibacterial; immunosuppressive; osteopathic; antidiabetic; antiasthmatic; analgesic; gene therapy.
KW neuromuscular; analgesic; gene therapy.
XX OS Mus musculus.
XX WO200164834-A2.
PD PD
FX 07-SEP-2001.
XX
PX 26-FEB-2001; 2001WO-US004926.
XX
PY 28-FEB-2000; 2000US-00515126.
PR 18-MAY-2000; 2000US-00577409.
PR 17-JUN-2000; 2000US-00597707.
PR 14-JUL-2000; 2000US-00616807.
PR 19-SEP-2000; 2000US-00664641.
XX
XX (HYSEQ-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;

XX WPI; 2001-589862/66.
XX N-PSDB; RAAS44641.

PT Novel peptides and nucleic acids obtained from cDNA libraries
prepared from various human tissues, for diagnosis, treatment of cancer,
neurological, inflammatory disorders and for use in arrays for detection.
XX

Claim 10; SEQ ID NO 238; 153pp; English.

Sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequences

Sequence 182 AA;

Query Match	65.04;	Score 580.5;	DB 4;	Length 182;
Best Local Similarity	81.14;	Pred. No. 3e-56;		
Matches 116;	Conservative 5;	Mismatches 9;	Indels 13;	Gaps 2;
Qy	1	MTTASTQVQRNVHDSERAINRQINLELYASVYLSMSVYFDRDDVALKNFAKVFYHQ	60	
Db	1	MTTASPQVQRNVHQDAEAINRQINLELYASVYLSMSVYFDRDDVALKNFAKVFYHQ	60	
Qy	61	HEERQAEKLMKLNQRGRIFLODIKKPCDDWESGLNAMECALHLEKNVQSILPP	120	
Db	61	HEEREAEKLMKLNQRGRIFLODIKKPDRDDWESGLNAMECALHLEKSVQSILEL	118	
Qy	121	PISPSPCSWHHYTNRPQPHHL	143	
Db	119	-----HKLATDKNDP--HL	130	

Search completed: March 30, 2005, 19:39:12
Job time : 80 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 19:37:13 ; Search time 16 Seconds
(without alignments)
992.235 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTSQVRQNYHQDSEA.....PRRRKRPHSIPTPIIRSP 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.5	68.9	183	1 FRHUH	ferritin heavy cha
2	580.5	65.0	141	2 I48109	ferritin heavy cha
3	580.5	65.0	182	2 S06070	ferritin heavy cha
4	573.5	64.2	181	2 A39884	ferritin heavy cha
5	560.5	62.8	180	2 A26886	ferritin heavy cha
6	499.5	55.9	164	2 I46710	ferritin heavy cha
7	439	49.2	174	2 S45603	ferritin, soma - g
8	424.5	47.5	176	1 FRXL	ferritin heavy cha
9	423	47.4	85	2 S68315	ferritin H chain -
10	423	47.4	176	2 A27805	ferritin chain H -
11	419	46.9	176	1 FRPGL	ferritin, tadpole
12	403.5	45.2	176	2 C27805	ferritin chain M -
13	401	44.9	174	2 B27805	ferritin chain L -
14	386	43.2	170	2 T33854	hypothetical prote
15	372	41.7	173	1 B45628	ferritin heavy cha
16	348	39.0	170	2 T31870	hypothetical prote
17	346	38.7	175	2 S01239	ferritin light cha
18	341	38.2	175	2 JC7238	ferritin protein l
19	341	38.2	183	1 FRTL	ferritin light cha
20	339	38.0	183	2 I54774	ferritin light cha
21	328.5	36.8	181	2 S62651	ferritin - signal
22	321	35.9	183	2 B33355	ferritin light cha
23	320	35.8	175	1 FRHOL	ferritin light cha
24	316	35.4	175	1 FRHUL	ferritin light cha
25	303	33.9	250	2 A40992	ferritin precursor
26	297.5	33.3	254	2 T08593	ferritin precursor
27	289	32.4	250	2 T08124	ferritin 2 precurs
28	288	32.3	250	1 FRFBH	ferritin heavy cha
29	287	32.1	259	2 G84827	probable ferritin

30	283	31.7	256	2 T08123	ferritin 3 precurs
31	282	31.6	285	2 S22498	ferritin precursor
32	281	31.5	253	2 S27358	ferritin precursor
33	280	31.4	300	2 S24057	ferritin 2 precurs
34	273.5	30.6	255	2 S71880	ferritin 1 precurs
35	268	30.0	172	1 A45628	ferritin heavy cha
36	266	29.8	259	2 T47726	hypothetical prote
37	187.5	21.0	239	2 S45604	ferritin precursor
38	186.5	20.9	173	2 B63354	ferritin homolog -
39	183	20.5	164	2 E72293	ferritin - Thermot
40	180.5	20.2	171	2 G69077	ferritin like prot
41	155	17.4	31	2 S04980	ferritin heavy cha
42	150	16.8	72	2 P06113	ferritin 5 - cowpe
43	145	16.2	49	2 S68314	ferritin L chain -
44	144	16.1	169	2 D83790	ferritin BHL124 [1
45	143	16.0	72	2 P06615	ferritin 1 - cowpe

ALIGNMENTS

RESULT 1

FRHUH

ferritin heavy chain - human

N:Alternate names: apoferritin H; ferritin heavy polypeptide 1

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence revision 31-Dec-1993 #text change 09-Jul-2004

C:Accession: A23517; A25045; JN0571; A23920; A24844; A03269; A05250; P05562

R:Costanzo, F.; Colombo, M.; Staempfli, S.; Santoro, C.; Marone, M.; Frank, R.; Delius, Nucleic Acids Res. 14, 721-736, 1986

A>Title: Structure of gene and pseudogenes of human apoferritin H.

A:Reference number: A23517; MUID:86120367; PMID:3003694

A:Accession: A23517

A:Molecule type: DNA

A:Residues: 1-183 <COS>

A:Cross-references: UNIPROT:P02794; GB:X03487; NID:G31340; PIDN:CAA27205.1; PID:G762940,

R:Hentze, M.W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi, W.; Drysdale, J.; Leonard, Proc. Natl. Acad. Sci. U.S.A. 83, 7226-7230, 1986

A>Title: Cloning, characterization, expression, and chromosomal localization of a human

A:Reference number: A25045; MUID:87016920; PMID:3020541

A:Accession: A25045

A:Molecule type: DNA

A:Residues: 1-183 <HEN>

A:Cross-references: GB:M14211; GB:M14212; NID:G182509; PIDN:AAA52438.1; PID:G182511; GB:R:Dhar, M.; Chauthaiwale, V.; Joshi, J.G. Gene 126, 275-278, 1993

A>Title: Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old human fet-

A:Reference number: JN0571; MUID:93246257; PMID:7916709

A:Accession: JN0571

A:Molecule type: mRNA

A:Residues: 1-183 <DHA>

A:Cross-references: GB:M97164; NID:G306743; PIDN:AAA35832.1; PID:G306744

R:Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W. J. Biol. Chem. 260, 11755-11761, 1985

A>Title: Structural and functional relationships of human ferritin H and L chains deduc-

A:Reference number: A32494; MUID:86008223; PMID:3840162

A:Accession: A32494

A:Molecule type: mRNA

A:Residues: 1-183 <BOY>

A:Cross-references: GB:M11146; NID:G182504; PIDN:AAA52437.1; PID:G182505 R:Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concannon, P.; Wong, A.; Chada, S.; Davis, R.C. Mol. Cell. Biol. 6, 586-593, 1986

A>Title: Structure and expression of ferritin genes in a human promyelocytic cell line

A:Reference number: A33087; MUID:87064341; PMID:3023856

A:Accession: A24844

A:Molecule type: mRNA

A:Residues: 1-183 <CHO>

A:Cross-references: GB:M12937; NID:G182506; PIDN:AAA35830.1; PID:G182507 R:Costanzo, F.; Santoro, C.; Colantuoni, V.; Bensi, G.; Raugel, G.; Romano, V.; Cortese, EMBO J. 3, 23-27, 1984

A>Title: Cloning and sequencing of a full length cDNA coding for a human apoferritin H

A:Reference number: A03269; MUID:84158535; PMID:6323167


```
Db 1 MTTASPSQVRQNYHQDAEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHQS 60
Qy 61 HEERHAEKLMKLNQGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
Db 61 HEERHAEKLMKLNQGRGRIPLQDIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-- 118
Qy 121 PISPSPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 4
ferritin heavy chain - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
C:Accession: A39884; A05251; A15903; I52222
R:Murray, M.T.; White, K.; Munro, H.N.
Proc. Natl. Acad. Sci. U.S.A. 84, 7438-7442, 1987
A:Title: Conservation of ferritin heavy subunit gene structure: implications for the reg
A:Reference number: A39884; MUID:88041121; PMID:3478702
A:Accession: A39884
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <MUR>
A:Cross-references: UNIPROT:P19132; GB:M18053; NID:G204126; PIDN:AAA41153.1; PID:G204128
R:Leibold, E.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.
J. Biol. Chem. 259, 4327-4334, 1984
A:Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer
A:Reference number: A92474; MUID:84162134; PMID:6546756
A:Accession: A05251
A:Molecule type: protein
A:Residues: 158-180, 'E' <LEI>
A:Experimental source: liver
R:Huberman, A.; Barahona, E.
Biochim. Biophys. Acta 533, 51-56, 1978
A:Title: Primary structure of rat liver apoferritin. The amino end.
A:Reference number: A15903; MUID:78144897; PMID:638195
A:Accession: A15903
A:Molecule type: protein
A:Residues: 4, 6-7 <HUB>
R:Ursini, M.V.; de Franciscis, V.
Biochem. Biophys. Res. Commun. 150, 287-295, 1988
A:Title: TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids.
A:Reference number: I52222; MUID:88106597; PMID:2827671
A:Accession: I52222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 136-181 <RES>
A:Cross-references: GB:M29330; NID:G207527; PIDN:AAA42300.1; PID:G207528
C:Superfamily: ferritin
C:Keywords: acetylated amino end; iron storage
P:4/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 64.2%; Score 573.5; DB 2; Length 181;
Best Local Similarity 81.0%; Pred. No. 1.3e-45;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

Qy 2 TTASTSQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHOSH 61
Db 1 TTASTSQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHOSH 60
Qy 62 EERHAEKLMKLNQGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPSP 121
Db 61 EERHAEKLMKLNQGRGRIPLQDIKKPDRDDWESGLNAMECALHLEKSNQSLLEL--- 117
Qy 122 ISPSPSCWHYTTNRPOQHHL 143
Db 118 -----HKLATDKNDP--HL 129

RESULT 5
ferritin heavy chain - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
C:Accession: A39884; A05251; A15903; I52222
R:Murray, M.T.; White, K.; Munro, H.N.
Proc. Natl. Acad. Sci. U.S.A. 84, 7438-7442, 1987
A:Title: Conservation of ferritin heavy subunit gene structure: implications for the reg
A:Reference number: A39884; MUID:88041121; PMID:3478702
A:Accession: A39884
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <MUR>
A:Cross-references: UNIPROT:P19132; GB:M18053; NID:G204126; PIDN:AAA41153.1; PID:G204128
R:Leibold, E.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.
J. Biol. Chem. 259, 4327-4334, 1984
A:Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer
A:Reference number: A92474; MUID:84162134; PMID:6546756
A:Accession: A05251
A:Molecule type: protein
A:Residues: 158-180, 'E' <LEI>
A:Experimental source: liver
R:Huberman, A.; Barahona, E.
Biochim. Biophys. Acta 533, 51-56, 1978
A:Title: Primary structure of rat liver apoferritin. The amino end.
A:Reference number: A15903; MUID:78144897; PMID:638195
A:Accession: A15903
A:Molecule type: protein
A:Residues: 4, 6-7 <HUB>
R:Ursini, M.V.; de Franciscis, V.
Biochem. Biophys. Res. Commun. 150, 287-295, 1988
A:Title: TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids.
A:Reference number: I52222; MUID:88106597; PMID:2827671
A:Accession: I52222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 136-181 <RES>
A:Cross-references: GB:M29330; NID:G207527; PIDN:AAA42300.1; PID:G207528
C:Superfamily: ferritin
C:Keywords: acetylated amino end; iron storage
P:4/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 64.2%; Score 573.5; DB 2; Length 181;
Best Local Similarity 81.0%; Pred. No. 1.3e-45;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

Qy 2 TTASTSQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHOSH 61
Db 1 TTASTSQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHOSH 60
Qy 62 EERHAEKLMKLNQGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPSP 121
Db 61 EERHAEKLMKLNQGRGRIPLQDIKKPDRDDWESGLNAMECALHLEKSNQSLLEL--- 117
Qy 122 ISPSPSCWHYTTNRPOQHHL 143
Db 118 -----HKLATDKNDP--HL 129
```

```
A26886
ferritin heavy chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A26886
R:Stevens, P.W.; Dodgson, J.B.; Engel, J.D.
Mol. Cell. Biol. 7, 1751-1758, 1987
A:Title: Structure and expression of the chicken ferritin H-subunit gene.
A:Reference number: A26886; MUID:87257874; PMID:3606643
A:Accession: A26886
A:Molecule type: DNA
A:Residues: 1-180 <STE>
A:Cross-references: UNIPROT:P08267; GB:M16343; NID:G211773; PIDN:AAA48768.1; PID:G211774
C:Genetics:
A:introns: 37/3; 86/3; 128/3
C:Superfamily: ferritin

Query Match 62.8%; Score 560.5; DB 2; Length 180;
Best Local Similarity 81.0%; Pred. No. 2e-44;
Matches 111; Conservative 3; Mismatches 10; Indels 13; Gaps 2;

Qy 7 SQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHQSHEERH 66
Db 6 SQVRQNYHQDSEAAINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHQSHEERH 65
Qy 67 AEKLMKLNQGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPSPISPS 126
Db 66 AEKLMKLNQGRGRIPLQDIKKPDRDDWENGLTAMECALHLEKNVNSLLEL----- 117
Qy 127 SCWHYTTNRPOQHHL 143
Db 118 ---HKLATDKNDP--HL 129

RESULT 6
I46710
ferritin heavy chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46710
R:Liau, G.; Chan, L.M.; Feng, P.
J. Biol. Chem. 266, 18819-18826, 1991
A:Title: Increased ferritin gene expression is both promoted by cAMP and a marker of gr
A:Reference number: I46677; MUID:92011647; PMID:1655764
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-164 <LIA>
A:Cross-references: UNIPROT:P25915; GB:M63912; NID:G165012; PIDN:AAA31247.1; PID:G16501
C:Superfamily: ferritin

Query Match 55.9%; Score 499.5; DB 2; Length 164;
Best Local Similarity 79.8%; Pred. No. 7.4e-39;
Matches 99; Conservative 5; Mismatches 7; Indels 13; Gaps 2;

Qy 20 AINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHQSHEERHQAELKLNQORGG 79
Db 1 AINRQINLELYASVYVLSMSCYFDRDDVALKNFAKYFLHQSHEERHQAELKLNQORGG 60
Qy 80 RIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPSPISPSCHYTTNRPOP 139
Db 61 RIFLQDIKKPDCDDWESGLNAMECALHLEKSNVNSLLEL-----HKLATDKNDP 109
Qy 140 QHHL 143
Db 110 ---HL 111

RESULT 7
S45603
ferritin, soma - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
```

C:Accession: S45603; S31358
 R: von Darl, M.; Harrison, P.M.; Bottko, W.
 Eur. J. Biochem. 222, 353-366, 1994
 A:Title: cDNA cloning and deduced amino acid sequence of two ferritins: soma ferritin and
 A:Reference number: S45603; MUID:94291629; PMID:7517354
 A:Accession: S45603
 A:Molecule type: mRNA
 A:Residues: 1-174 <VON>
 A:Cross-references: UNIPROT:P42577; EMBL:X56778; NID:g9649; PIDN:CAA40096.1; PID:g9650
 A:Experimental source: adult; visceral mass
 A:Note: in the authors' translation 134-Glu is not shown, residues 135-141 are displaced
 C:Complex: functional molecule is composed of 24 chains
 C:Function:
 A:Description: intracellular protein that stores and transports iron in a soluble, nontoxic
 C:Superfamily: ferritin
 C:Keywords: iron; iron binding; iron storage; iron transport; metalloprotein
 F:25,59,60,62,63,105/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted
 F:82/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted
 F:84/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match 49.2%; Score 439; DB 2; Length 174;
 Best Local Similarity 74.3%; Pred. No. 3e-33;
 Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 5 STSQVRYHQDSEAINRQINLELYASYVLSMSYFFDRDDVALKNFAKFLHQSHEER 64
 Db 2 SVSQARQNYHAESEAGINRQINMELYASYQSMAYFFDRDDVALPGPHKFFKHQSEER 61

Qy 65 QHAEKLMKLNQGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLE 117
 Db 62 EHAELKMLYQNKGRGRIVLQDIKKPDRDEWGTGLEAMQVALQLEKSVNSQLLD 114

RESULT 8
 FXLL
 ferritin heavy chain - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1991 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: A37959; S12463; S09499; A40408
 R:Holland, L.J.; Wall, A.A.; Bhattacharya, A.
 Biochemistry 30, 1965-1972, 1991
 A:Title: Xenopus liver ferritin H subunit: cDNA sequence and mRNA production in the liver
 A:Reference number: A37959; MUID:91129281; PMID:1993207
 A:Accession: A37959
 A:Molecule type: mRNA
 A:Residues: 1-176 <HOL>
 A:Cross-references: UNIPROT:P17663; GB:M55010; NID:g214135; PIDN:AAA49708.1; PID:g214136
 A:Experimental source: liver
 R:Schoenberg, D.
 submitted to the EMBL Data Library, January 1990
 A:Reference number: S12463
 A:Accession: S12463
 A:Molecule type: mRNA
 A:Residues: 1-5, 'L', 7-14, 'I', 16-156, 'A', 159-176 <SCH>
 A:Cross-references: EMBL:X51395; NID:g64690; PIDN:CAA35760.1; PID:g64691
 R:Moskaitis, J.E.; Pastori, R.L.; Schoenberg, D.R.
 Nucleic Acids Res. 18, 2184, 1990
 A:Title: Sequence of Xenopus laevis ferritin mRNA.
 A:Reference number: S09499; MUID:90245677; PMID:2336402
 A:Accession: S09499
 A:Molecule type: mRNA
 A:Residues: 1-5, 'L', 7-14, 'I', 16-64, 70-86, 'KFLKY', 87-156, 'A', 159-176 <MOS>
 A:Cross-references: EMBL:X51395
 A:Note: the sequence shown in the alignment is inconsistent with the nucleotide sequence
 R:Muller, J.P.; Vedel, M.; Monnot, M.J.; Touzet, N.; Wegnez, M.
 DNA Cell Biol. 10, 571-579, 1991
 A:Title: Molecular cloning and expression of ferritin mRNA in heavy metal-poisoned Xenopus
 A:Reference number: A40408; MUID:92029619; PMID:1718317
 A:Accession: A40408
 A:Molecule type: mRNA
 A:Residues: 1-9, 'H', 11-22, 'W', 24-90, 'G', 92-96, 'T', 98-123, 'AH', 126-143, 'Q', 145-176 <MUL>
 A:Cross-references: EMBL:X64727
 A:Experimental source: cadmium-poisoned XL2 embryonic cell line

C:Complex: The functional molecule is composed of 24 chains, is roughly spherical and co
 C:Function:
 A:Description: intracellular protein that stores and transports iron in a soluble, nontoxic
 C:Superfamily: ferritin
 C:Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer
 F:24,58,59,61,62,104/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted
 F:81/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted
 F:83/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match 47.5%; Score 424.5; DB 1; Length 176;
 Best Local Similarity 60.4%; Pred. No. 6.5e-32;
 Matches 81; Conservative 19; Mismatches 23; Indels 11; Gaps 1;

Qy 7 SQVQRYHQDSEAINRQINLELYASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQH 66
 Db 3 SQVQRYHQDSEAINRQINLELYASYVLSMSYFFDRDDVALHVAKFFKEQSHEREH 62

Qy 67 AEKLMKLNQGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSPISPS 126
 Db 63 AEKFLKYQNKGRGRIVLQDIKKPDRDEWSNTLEAMQALQLEKTVNQALLDL----- 114

Qy 127 SCWHYTTNRPQPQ 140
 Db 115 ---HKLASDKVDPQ 125

RESULT 9
 S68315
 ferritin H chain - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
 C:Accession: S68315
 R:Gosiewska, A.; Mahmoodian, F.; Peterkofsky, B.
 Arch. Biochem. Biophys. 325, 295-303, 1996
 A:Title: Gene expression of iron-related proteins during iron deficiency caused by scur
 A:Reference number: S68313; MUID:96139112; PMID:8561510
 A:Accession: S68315
 A:Molecule type: mRNA
 A:Residues: 1-85 <GOS>
 A:Cross-references: GB:S91307; NID:g1336695; PIDN:AAB35970.1; PID:g1336696
 C:Superfamily: ferritin

Query Match 47.4%; Score 423; DB 2; Length 85;
 Best Local Similarity 94.1%; Pred. No. 3.7e-32;
 Matches 80; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 31 ASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQHAELKLMKLNQGRIFLODIKKPD 90
 Db 1 ASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQHAELKLMKLNQGRIFLODIKKPD 60

Qy 91 CDDWESGLNAMECALHLEKNVNSL 115
 Db 61 RDDWENGLNAMECALHLEKSVNSL 85

RESULT 10
 A27805
 ferritin chain H - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
 C:Accession: A27805
 R:Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
 J. Biol. Chem. 262, 7901-7907, 1987
 A:Title: Differences in the regulation of messenger RNA for housekeeping and specialized
 A:Reference number: A92648; MUID:87222424; PMID:3495534
 A:Accession: A27805
 A:Molecule type: mRNA
 A:Residues: 1-176 <DIC>
 A:Cross-references: UNIPROT:P07229; GB:M15655; NID:g213672; PIDN:AAA49523.1; PID:g213673
 C:Superfamily: ferritin

Query Match 47.4%; Score 423; DB 2; Length 176;
Best Local Similarity 70.3%; Pred. No. 9e-32;
Matches 78; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 117
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 113

RESULT 11
ferritin, tadpole - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A25627
R:Dickey, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.
J. Biol. Chem. 261, 949-955, 1986
A>Title: Multiple red cell ferritin mRNAs, which code for an abundant protein in the embryo
A:Reference number: A25627; MUID:86085940; PMID:3484480
A:Accession: A25627
A:Molecule type: mRNA
A:Residues: 1-176 <DID>
A:Cross-references: UNIPROT:P07229; GB:M12120; NID:G213691; PIDN:AAA49532.1; PID:G213692
A:Experimental source: reticulocytes
C:Comment: The sequence of this ferritin is more similar to mammalian H chains than to I
C:Superfamily: ferritin
C:Keywords: erythrocyte; iron storage

Query Match 46.9%; Score 419; DB 1; Length 176;
Best Local Similarity 69.4%; Pred. No. 2.1e-31;
Matches 77; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 117
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 113

RESULT 12
ferritin chain M - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: C27805
R:Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.
J. Biol. Chem. 262, 7901-7907, 1987
A>Title: Differences in the regulation of messenger RNA for housekeeping and specialized
n-tification of the first processed pseudogene in amphibia.
A:Reference number: A26648; MUID:87222424; PMID:3495534
A:Accession: C27805
A:Molecule type: mRNA
A:Residues: 1-176 <DIC>
A:Cross-references: UNIPROT:P07798; GB:J02724; NID:G213676; PIDN:AAA49525.1; PID:G213677
C:Superfamily: ferritin

Query Match 45.2%; Score 403.5; DB 2; Length 176;
Best Local Similarity 58.4%; Pred. No. 5.6e-30;
Matches 80; Conservative 16; Mismatches 28; Indels 13; Gaps 2;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLEPSP 126
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLEPSP 114

QY 127 SCWHYTTNRQPQHLL 143
DB 115 ---HKLATDKVDP--HL 126

RESULT 13

B27805

ferritin chain L - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 16-Aug-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993

C:Accession: B27805

R:Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.

J. Biol. Chem. 262, 7901-7907, 1987

A>Title: Differences in the regulation of messenger RNA for housekeeping and specialized

n-tification of the first processed pseudogene in amphibia.

A:Reference number: A92648; MUID:87222424; PMID:3495534

A:Accession: B27805

A:Molecule type: mRNA

A:Residues: 1-174 <DIC>

C:Superfamily: ferritin

Query Match 44.9%; Score 401; DB 2; Length 174;
Best Local Similarity 64.0%; Pred. No. 9.4e-30;
Matches 71; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66

DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDVALKNFAKYFLHQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 117

DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLE 113

RESULT 14

T33854

hypothetical protein D1037.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33854

R:Ledwith, J.; Biewald, T.

submitted to the EMBL Data Library, November 1998

A>Description: The sequence of C. elegans cosmid D1037.

A:Reference number: Z21424

A:Accession: T33854

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-170 <LED>

A:Cross-references: UNIPROT:Q9TYS3; EMBL:AF106592; PIDN:AAC78491.1; GSPDB:GNO0019; CESP

A:Experimental source: strain Bristol N2; clone D1037

C:Genetics:

A:Gene: CESP:D1037.3

A:Map position: 1

A:Introns: 19/3; 137/3

C:Superfamily: ferritin

Query Match 43.2%; Score 386; DB 2; Length 170;
Best Local Similarity 64.9%; Pred. No. 2.2e-28;
Matches 74; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66

DB 2 SLARQNYHSEAAVKNQINLELYASYVLSMSYFFDRDDVALPNIAKFFKEQSDEERH 61

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVNSILLEPSP 120

DB 62 ATELNRVQLRGRVLLQDIORPENDEMGTKALKAFAALALEKFNNESULLKHS 115

RESULT 15

B45628

ferritin heavy chain 1 - fluke (Schistosoma mansoni)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:37:59 ; Search time 52 Seconds
(without alignments)
1050.609 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTQVRQYHQDSEAA.....PRRRKRPHSIPTLIRSP 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	615.5	68.9	183	15	US-10-384-496-2
2	615.5	68.9	183	17	US-10-734-049A-231
3	615.5	68.9	190	15	US-10-435-666-8
4	615.5	68.9	190	16	US-10-734-564-127
5	583.5	65.3	182	15	US-10-384-496-12
6	580.5	65.0	182	15	US-10-384-496-6
7	579.5	64.9	180	14	US-10-324-153-4
8	523.5	58.6	127	15	US-10-264-049-3406
9	494	55.3	242	14	US-10-324-153-2
10	477	53.4	173	15	US-10-216-464-29
11	400.5	44.8	121	15	US-10-042-865-176
12	399	44.7	183	9	US-09-801-574-70
13	390.5	43.7	183	15	US-10-092-900A-260

14	387.5	43.4	204	16	US-10-478-758-9	Sequence 9, Appli
15	379.5	42.5	178	14	US-10-029-386-32858	Sequence 32858, A
16	375.5	42.0	221	9	US-09-801-574-68	Sequence 68, Appli
17	361	40.4	85	9	US-09-925-302-812	Sequence 812, App
18	361	40.4	85	10	US-09-925-302-812	Sequence 812, App
19	343	38.4	199	16	US-10-363-829-400	Sequence 400, App
20	341	38.2	183	15	US-10-384-496-14	Sequence 14, Appli
21	338	37.8	175	15	US-10-042-865-172	Sequence 172, App
22	338	37.8	183	15	US-10-384-496-10	Sequence 10, Appli
23	338	37.8	183	15	US-10-042-865-175	Sequence 175, App
24	335	37.5	183	15	US-10-042-865-173	Sequence 173, App
25	325.5	36.5	175	15	US-10-042-865-171	Sequence 171, App
26	321	35.9	183	15	US-10-384-496-8	Sequence 8, Appli
27	320	35.8	175	15	US-10-042-865-174	Sequence 174, App
28	316	35.4	175	10	US-09-919-039-333	Sequence 333, App
29	316	35.4	175	15	US-10-435-666-4	Sequence 4, Appli
30	316	35.4	175	15	US-10-262-445-56	Sequence 56, Appli
31	316	35.4	175	16	US-10-734-564-128	Sequence 128, App
32	316	35.4	254	15	US-10-104-047-3198	Sequence 3198, Ap
33	315	35.3	176	9	US-09-801-574-28	Sequence 28, Appli
34	312	34.9	154	14	US-10-029-386-29603	Sequence 29603, A
35	303	33.9	250	15	US-10-424-599-184909	Sequence 184909,
36	298	33.4	262	15	US-10-425-114-62139	Sequence 62139, A
37	298	33.4	262	15	US-10-425-114-63725	Sequence 63725, A
38	295	33.0	249	15	US-10-424-599-147651	Sequence 147651,
39	294	32.9	250	9	US-09-834-624-2	Sequence 2, Appli
40	294	32.9	250	9	US-09-834-624-3	Sequence 3, Appli
41	292	32.7	248	15	US-10-424-599-278212	Sequence 278212,
42	292	32.7	262	15	US-10-425-114-63721	Sequence 63721, A
43	292	32.7	262	15	US-10-425-114-63723	Sequence 63723, A
44	291	32.6	167	16	US-10-617-955-2	Sequence 2, Appli
45	291	32.6	167	16	US-10-617-955-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-384-496-2
; Sequence 2, Application US/10384496
; Publication No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: AHRENS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND
; TITLE OF INVENTION: METHODS RELATED THERETO
; FILE REFERENCE: CMV-001.01
; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-496-2

Query Match	68.9%	Score 615.5;	DB 15;	Length 183;
Best Local Similarity	84.6%	Pred. No. 6.1e-55;		
Matches 121;	Conservative 3;	Mismatches 6;	Indels 13;	Gaps 2;
Qy	1	MTTASTQVRQYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVAKNPKFYFLHQ5	60	
Db	1	MTTASTQVRQYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVAKNPKFYFLHQ5	60	
Qy	61	HEERQHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPP5	120	
Db	61	HEERHAELKMLQNGRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPP5	118	
Qy	121	PISPSPCWHYTTNRPOPHHL	143	
Db	119	-----HKLATDKNDP--HL	130	

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RESULT 2
US-10-734-049A-231
; Sequence 231, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; APPLICANT: SHICHIGO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734,049A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/JP02/05799
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001/177058
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001/250728
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 231
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-049A-231

Query Match      68.9%; Score 615.5; DB 17; Length 183;
Best Local Similarity 84.6%; Pred. No. 6.1e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

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Db      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60

Qy      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
Db      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120

Qy      121 PISPPSCWHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130

RESULT 3
US-10-435-666-8
; Sequence 8, Application US/10435666
; Publication No. US20040006001A1
; GENERAL INFORMATION:
; APPLICANT: CARTER, Daniel C.
; TITLE OF INVENTION: FERRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATIONS
; FILE REFERENCE: P07624W00/BAS
; CURRENT APPLICATION NUMBER: US/10/435,666
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,145
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-666-8

Query Match      68.9%; Score 615.5; DB 15; Length 190;
Best Local Similarity 84.6%; Pred. No. 6.4e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

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Db      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60

Qy      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
Db      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120

Qy      121 PISPPSCWHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130
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Db      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 118

Qy      121 PISPPSCWHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130

RESULT 4
US-10-734-564-127
; Sequence 127, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-127

Query Match      68.9%; Score 615.5; DB 16; Length 190;
Best Local Similarity 84.6%; Pred. No. 6.4e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

Qy      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60

Qy      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
Db      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 118

Qy      121 PISPPSCWHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130

RESULT 5
US-10-384-496-12
; Sequence 12, Application US/10384496
; Publication No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: AHRENS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND METHODS RELATED THERETO
; FILE REFERENCE: CMV-001.01
; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-384-496-12

Query Match      65.3%; Score 583.5; DB 15; Length 182;
Best Local Similarity 81.8%; Pred. No. 1.2e-51;
Matches 117; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

Qy      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db      1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60

Qy      61 HEERQHAELKMLQNRGRIFLQDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS 120
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Db 61 HEERHAELKMLQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-- 118
QY 121 PISPSPCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 6

US-10-384-496-6
; Sequence 6, Application US/10384496
; Publication No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: AHERNS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND
; TITLE OF INVENTION: METHODS RELATED THERETO
; FILE REFERENCE: CMV-001.01
; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-496-6

Query Match 65.0%; Score 580.5; DB 15; Length 182;
Best Local Similarity 81.1%; Pred. No. 2.4e-51;
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
Db 1 MTASTSQVRQNYHQDAEAANRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
QY 61 HEERHAELKMLQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPFS 120
Db 61 HEERHAELKMLQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-- 118
QY 121 PISPSPCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 7

US-10-324-153-4
; Sequence 4, Application US/10324153
; Publication No. US20030114645A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000843CON
; CURRENT APPLICATION NUMBER: US/10/324,153
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Trichosurus vulpecula
US-10-324-153-4

Query Match 64.9%; Score 579.5; DB 14; Length 180;
Best Local Similarity 82.1%; Pred. No. 2.9e-51;
Matches 115; Conservative 4; Mismatches 8; Indels 13; Gaps 2;

QY 4 ASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEE 63
Db 1 SSPSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEE 60

QY 64 ROHAELKMLQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPSPIS 123
Db 61 REHAELKMLQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL----- 115
QY 124 PPSPCWHYTTNRPOQHHL 143
Db 116 -----HKLATDKNDP--HL 127

RESULT 8

US-10-264-049-3406
; Sequence 3406, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAJ33PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 3406
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3406

Query Match 58.6%; Score 523.5; DB 15; Length 127;
Best Local Similarity 82.4%; Pred. No. 1.1e-45;
Matches 103; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEEROHAELKMLQNGR 78
Db 1 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEEROHAELKMLQNGR 60
QY 79 GRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPSPISPCWHYTTNRPQ 138
Db 61 GRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-----HKLATDKND 109
QY 139 POHHL 143
Db 110 P--HL 112

RESULT 9

US-10-324-153-2
; Sequence 2, Application US/10324153
; Publication No. US20030114645A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000843CON
; CURRENT APPLICATION NUMBER: US/10/324,153
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Human
US-10-324-153-2

Query Match 55.3%; Score 494; DB 14; Length 242;
Best Local Similarity 83.3%; Pred. No. 2.5e-42;
Matches 95; Conservative 9; Mismatches 10; Indels 0; Gaps 0;


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; PRIOR APPLICATION NUMBER: 60/187,518
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/261,557
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-70

Query Match          44.7%; Score 399; DB 9; Length 183;
Best Local Similarity 65.0%; Pred. No. 1e-32;
Matches 76; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTTASTQVRQNYHDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db 1 MATAQPSQVRQKYDNTCDAAINSHITLTYLSYLSMAFYFNRRDDVALENPFYFLRLS 60

QY 61 HEERQHAELKMLQNRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLE 117
Db 61 DDKMEHAQKMLQNLRGGHICLHDIRKPEQGWESGLVAMESAPFHLEKNVNSLLE 117

RESULT 13
US-10-092-900A-260
; Sequence 260, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
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; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 260
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-260

Query Match          43.7%; Score 390.5; DB 15; Length 183;
Best Local Similarity 56.7%; Pred. No. 7.4e-32;
Matches 76; Conservative 17; Mismatches 30; Indels 11; Gaps 1;

QY 7 SOVRQNYHDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQSHEERH 66
Db 7 SPVRYHHPSCAAINTHISLEHPSYVYLSMAFYFDDDDAALEHFDYFLQSQSEKREH 66

QY 67 AEKLMKLNQNRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPSPSP 126
Db 67 AQELMSLQNLRRGGRICLHDIRKPEQGWESGLKAMECTFHLEKNINQSLLE----- 118

QY 127 SCWHYTTNRFPQP 140
Db 119 ---HQLARENGDPQ 129

RESULT 14
US-10-478-758-9
; Sequence 9, Application US/10478758
; Publication No. US20040152874A1
; GENERAL INFORMATION:
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: BATRA, Sajeev
; APPLICANT: YAO, Monique G.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: RAMKUMAR, Javalaxmi
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LAL, Preeti G.
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: BECHA, Shanya D.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: CHINN, Anna M.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-0980 USN
; CURRENT APPLICATION NUMBER: US/10/478,758
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/US02/16446
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,722
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/296,881
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/304,593
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,105
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;; PRIOR FILING DATE: 2001-07-12
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: PERL Program
;; SEQ ID NO 9
;; LENGTH: 204
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No: 7486339CD1
US-10-478-758-9

Query Match 43.4%; Score 387.5; DB 16; Length 204;
Best Local Similarity 55.8%; Pred. No. 1.7e-31;
Matches 77; Conservative 19; Mismatches 31; Indels 11; Gaps 1;

QY 3 TASTQVRQNYHODSEAINRQINIELYASVYILSMYSYFDRDDVALKNFAKYFLHQSH 62
DB 36 TAPLQVRQNYHPDCDAAVSHVNLELHASCYLSMAFYLDVDRDVTLEFRFCFLSQSQ 95
QY 63 ERQHAELKMLQNRQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSQLLEFPSP 122
DB 96 KREHAQLMLQNLQGRICLDIWKPEREYWESGLQMECAFHLEESVNSLLEL----- 151
QY 123 SPSPSCWHYTTNRPOQ 140
DB 152 -----HYLAMEKGDPO 162

RESULT 15
US-10-029-386-32858
;; Sequence 32858, Application US/10029386
;; Publication No. US20030194704A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
;; FILE REFERENCE: AEWICA-X-2
;; CURRENT APPLICATION NUMBER: US/10/029,386
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 34288
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 32858
;; LENGTH: 178
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AJ239329.2
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.99
;; OTHER INFORMATION: SWISSPROT HIT: P02794, EVALUATE 4.00e-62
US-10-029-386-32858

Query Match 42.5%; Score 379.5; DB 14; Length 178;
Best Local Similarity 57.0%; Pred. No. 9.7e-31;
Matches 73; Conservative 16; Mismatches 28; Indels 11; Gaps 1;

QY 13 YHODSEAINRQINIELYASVYILSMYSYFDRDDVALKNFAKYFLHQSHERQHAELKMK 72
DB 2 HHPSCAAINTHISLELHASVYILSMAYFYQDDDALEHDFRYFLRQSQEKREHAQELMS 61
QY 73 LQNRQGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSQLLEFPSPSPSCWHY 132
DB 62 LQNLQGRICLDIRKPEQGWESGLKAMECTFHLEKNINQSLLEL-----HQL 110
QY 133 TTNRPQ 140

Db 111 ARENGDPQ 118

Search completed: March 30, 2005, 19:43:56
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:34:31 ; Search time 22 Seconds
(without alignments)
559.868 Million cell updates/sec

Title: US-09-786-867C-5
Perfect score: 893
Sequence: 1 MTTASTQVRQNYHQDSEAA.....PRRKRPHSIPTILIRSP 165

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615.5	68.9	220	4	US-09-949-016-10773 Sequence 10773, A
2	316	35.4	175	4	US-09-919-039-333 Sequence 333, App
3	312	34.9	238	4	US-09-949-016-10295 Sequence 10295, A
4	294	32.9	250	4	US-09-418-830-2 Sequence 2, Appli
5	294	32.9	250	4	US-09-418-830-3 Sequence 3, Appli
6	293.5	32.9	107	4	US-09-621-976-4402 Sequence 4402, Ap
7	177	19.8	243	2	US-08-829-110-3 Sequence 3, Appli
8	140.5	15.7	168	3	US-09-134-001C-4664 Sequence 4664, Ap
9	113.5	12.7	162	4	US-09-602-777A-362 Sequence 362, App
10	113	12.7	168	4	US-09-543-681A-7822 Sequence 7822, Ap
11	96.5	10.8	173	3	US-08-818-112-82 Sequence 82, Appli
12	96.5	10.8	173	3	US-08-818-111-83 Sequence 83, Appli
13	96.5	10.8	173	3	US-09-056-556-82 Sequence 83, Appli
14	96.5	10.8	173	4	US-09-072-596-83 Sequence 82, Appli
15	96.5	10.8	173	4	US-09-072-967-82 Sequence 82, Appli
16	96.5	10.8	181	4	US-09-050-739-54 Sequence 54, Appli
17	87	9.7	615	4	US-09-805-455-2 Sequence 2, Appli
18	83	9.3	709	4	US-09-949-016-6809 Sequence 6809, Ap
19	83	9.3	728	4	US-09-949-016-7213 Sequence 7213, Ap
20	82.5	9.2	534	4	US-09-248-796A-15937 Sequence 15937, A
21	81.5	9.1	1332	4	US-09-270-767-59785 Sequence 59785, A
22	81.5	9.1	1607	4	US-09-270-767-44362 Sequence 44362, A
23	80.5	9.0	337	4	US-09-252-991A-17436 Sequence 17436, A
24	79.5	8.9	1057	4	US-09-428-156B-2 Sequence 2, Appli
25	79	8.8	741	4	US-09-949-016-11523 Sequence 11523, A
26	79	8.8	741	4	US-09-949-016-11524 Sequence 11524, A
27	77.5	8.7	1001	3	US-09-060-410-2 Sequence 2, Appli

28	77.5	8.7	1001	4	US-09-723-458-2 Sequence 2, Appli
29	77	8.6	349	3	US-09-459-774-2 Sequence 2, Appli
30	77	8.6	349	4	US-09-417-039-7 Sequence 7, Appli
31	77	8.6	349	4	US-09-903-817-2 Sequence 2, Appli
32	77	8.6	372	4	US-09-949-016-8710 Sequence 8710, Ap
33	76.5	8.6	608	4	US-09-805-455-6 Sequence 6, Appli
34	76	8.5	182	4	US-09-252-991A-17493 Sequence 17493, A
35	76	8.5	462	4	US-09-949-016-6750 Sequence 6750, Ap
36	76	8.5	626	4	US-09-949-016-6749 Sequence 6749, Ap
37	76	8.5	778	4	US-09-949-016-6210 Sequence 6210, Ap
38	75.5	8.5	1037	4	US-09-252-991A-25361 Sequence 25361, A
39	75	8.4	432	4	US-09-583-110-4367 Sequence 4367, Ap
40	75	8.4	434	4	US-09-107-433-3684 Sequence 3684, Ap
41	74.5	8.3	786	4	US-09-688-188B-23 Sequence 23, Appli
42	74.5	8.3	786	4	US-09-291-417D-23 Sequence 23, Appli
43	74.5	8.3	787	4	US-09-688-188B-151 Sequence 151, App
44	74.5	8.3	787	4	US-09-291-417D-151 Sequence 151, App
45	74.5	8.3	1001	4	US-09-688-188B-31 Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-10773
; Sequence 10773: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10773
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10773

Query Match 68.9%; Score 615.5; DB 4; Length 220;
Best Local Similarity 84.6%; Pred No. 1.6e-61;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;
QY 1 MTTASTQVRQNYHQDSEAAINRQINLELYASYVYLSMSYVYFDRDDVALKNFAKYPFHQS 60
Db 38 MTTASTQVRQNYHQDSEAAINRQINLELYASYVYLSMSYVYFDRDDVALKNFAKYPFHQS 97
QY 61 HEERQAEKMKLQNGRGRIFLQIKKPCDDWESGLNAMECALHLEKNVQSLLEFPS 120
Db 98 HEERQAEKMKLQNGRGRIFLQIKKPCDDWESGLNAMECALHLEKNVQSLLEFPS 155
QY 121 PISPSPCWHYTTNRPOQHHL 143
Db 156 -----HKLATKNDP---HL 167

RESULT 2

US-09-919-039-333
; Sequence 333: Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US

```
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 333
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6727066 4005778CD1
US-09-919-039-333

Query Match          35.4%; Score 316; DB 4; Length 175;
Best Local Similarity 53.6%; Pred. No. 9.4e-28;
Matches 60; Conservative 22; Mismatches 30; Indels 0; Gaps 0;

Qy 6 TSQVRQNYHQDSEAAINRQINLELYASVYVLSMSYFDRDDVALKXNFAKYLHQSHHEEQ 65
Db 2 SSQIRQNSTDVEAAVNSLVNLYLOASTYLSLGFYFDRDDVALEGVSHFFRELAEKRE 61

Qy 66 HAEKLMKLNQGRGRIFLQDKKPCDDWESGLNAMECALHLEKNVNSLLE 117
Db 62 GYERLLKNQNGRGRALFQDIKKPAEDWEGKTPDAMKAAMALEKKNQALLD 113

RESULT 3
US-09-949-016-10295
; Sequence 10295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10295
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10295

Query Match          34.9%; Score 312; DB 4; Length 238;
Best Local Similarity 52.7%; Pred. No. 4.1e-27;
Matches 59; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TSQVRQNYHQDSEAAINRQINLELYASVYVLSMSYFDRDDVALKXNFAKYLHQSHHEEQ 65
Db 65 SSQIRQNSTDVEAAVNSLVNLYLOASTYLSLGFYFDRDDVALEGVSHFFRELAEKRE 124

Qy 66 HAEKLMKLNQGRGRIFLQDKKPCDDWESGLNAMECALHLEKNVNSLLE 117
Db 125 GYERLLKNQNGRGRALFQDIKKPAEDWEGKTPDAMKAAMALEKKNQALLD 176

RESULT 4
US-09-418-830-2
; Sequence 2, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: we do not have
; OTHER INFORMATION: this information
US-09-418-830-3

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;
```

```
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-418-830-2

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;

Qy 5 STSQVRQNYHQDSEAAINRQINLELYASVYVLSMSYFDRDDVALKXNFAKYLHQSHHEEQ 64
Db 77 NVSLARQNYQDEVSAINEQINVEYNVSYVYHSLFAYFDRDNVALKGLAKTFKESSEER 136

Qy 65 QHAEKLMKLNQGRGRIFLQDKKPCDDWESGLNAMECALHLEKNVNSLLEFPS 120
Db 137 EBAEKLMKYQNGRGRVVIHPIVSPPEFDBAEKGDALYAMELALSLEKLVNEKLVNHS 196

RESULT 5
US-09-418-830-3
; Sequence 3, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: we do not have
; OTHER INFORMATION: this information
US-09-418-830-3

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
```

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Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;
QY 5 STSVQRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHHEER 64
Db 77 NVSLARQNYQDEVSAINEQINVEYNVSYVLSLFPAYFDRDVALKGLAKFPKESSEER 136
QY 65 QHAEKLMKLNQGRGRIFLQDIKFP--DCDDWESG--LNAMECALHLEKNVNSLLEPPS 120
Db 137 EHAELMKYQINRGRVGVVHLFIVSPSPFDHAEKGDALYAMELASLSLEKLVNEKLLNVHS 196

RESULT 6
US-09-621-976-4402
; Sequence 4402, Application US/09621976
; Patent No. 6839063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4402
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4402

Query Match 32.9%; Score 293.5; DB 4; Length 107;
Best Local Similarity 53.8%; Pred. No. 1.7e-25;
Matches 56; Conservative 19; Mismatches 24; Indels 5; Gaps 2;
QY 38 MSYFDRDDVALKNFAKYLHQSHHEEROHAEKLMKLNQGRGRIFLQDIKPKDCDDWESG 97
Db 1 MAFFERDDVALEHFGRIYFLHQSDKMEHAQELMKLNQGRGRICLHDIREPQGWQSG 60
QY 98 LNAMECALHLEKNVNSLLEPPSPFI--SPSPSC---WHHYTTNR 136
Db 61 LEAMECAPHLEKSINYSLELHQLALEKGFSCATSWRATTLHQ 104

RESULT 7
US-08-829-110-3
; Sequence 3, Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; TITLE OF INVENTION: SIGNALING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0259 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYMNOT02
; CLONE: 343504
US-08-829-110-3

Query Match 19.8%; Score 177; DB 2; Length 243;
Best Local Similarity 36.0%; Pred. No. 8.1e-12;
Matches 45; Conservative 19; Mismatches 41; Indels 20; Gaps 3;
QY 6 TSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHHEERQ 65
Db 2 SSQIRQNYSTDVEAAVNSLVNLYLQASVYLSLGFYFDRDDVALEGVSHFFRELAEERQ 61
QY 66 HAEKLMKLNQGRGRIFLQDIK---KPCDDWESGLNAMECALHLEKNVN-----OSLLE 117
Db 62 -----GLRASPEDAKPAWRPPSDIHDGSSSSHQSLKSTAKWAASLENLLE 109
QY 118 FPSPI 122
Db 110 DPEGV 114

RESULT 8
US-09-134-001C-4664
; Sequence 4664, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4664
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4664

Query Match 15.7%; Score 140.5; DB 3; Length 168;
Best Local Similarity 32.6%; Pred. No. 6.5e-08;
Matches 31; Conservative 23; Mismatches 38; Indels 3; Gaps 2;
QY 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHHEERQHAELMKLNQGRG 78
Db 10 AALNEQNMNQYFAAHAYMAAAYCDKE--SYDGFANFYIEQAKBERPHGKKIYINDRG 67
QY 79 GRIFLQDIKPKDCDDWESGLNAMECALHLEKNVQ 113
Db 68 EHAIFDTIKAPKV-EFSSILETFKDSLAQERDVTQ 101

RESULT 9
US-09-602-777A-362
; Sequence 362, Application US/09602777A
```

; Patent No. 6831165
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelder, Oskar
 ; APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 ; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
 ; FILE REFERENCE: BGI-128CP
 ; CURRENT APPLICATION NUMBER: US/09/602.777A
 ; CURRENT FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 60/141031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: DE 19931636.8
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 199332125.6
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932126.4
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932127.2
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932128.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932129.9
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: DE 19932226.0
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: DE 19932920.6
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932922.2
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932924.9
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932928.1
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932930.3
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932933.8
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932935.4
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19932973.7
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933002.6
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933003.4
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933005.0
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19933006.9
 ; PRIOR FILING DATE: 1999-07-14
 ; PRIOR APPLICATION NUMBER: DE 19941378.9
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19941379.7
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19941390.8
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19941391.6
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: DE 19942088.2
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 442
 ; SEQ ID NO 362
 ; LENGTH: 162
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 ; US-09-602-777A-362

Query Match 12.7%; Score 113.5; DB 4; Length 162;
Best Local Similarity 33.3%; Pred. No. 7.1e-05;
Matches 33; Conservative 15; Mismatches 48; Indels 3; Gaps 2;

Qy	19	A	A	I	N	R	O	I	N	E	L	V	S	Y	F	D	R	D	V	A	L	K	F	A	K	F	L	H	S	H	E	R	O	H	A	E	K	M	L	K	N	O	R	G		78
Db	9	S	A	P	N	N	O	T	A	E	L	S	A	S	W	I	L	S	Y	L	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	66		
Qy	79	G	R	I	F	L	O	D	I	K	P	C	D	D	W	E	S	I	N	A	M	E	C	A	L	H	L	E	K	N	V	N	O	S	L	L	E		117							
Db	67	Y	P	O	I	G	D	I	A	P	P	K	L	-	D	V	T	S	A	I	E	A	F	E	A	S	L	A	E	O	K	I	S	L	A	I	R	E		104						

RESULT 10

```

US-09-543-681A-7822
; Patent 7822, Application US/09543681A
; Sequence No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; ACID COMPOSITIONS FOR DIAGNOSTICS AND THERA
; PEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7822
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7822

```

Query Match 12.7%; Score 113; DB 4; Length 168;
Best Local Similarity 32.9%; Pred. No. 8.5e-05;
Matches 26; Conservative 13; Mismatches 38; Indels 2; Gaps 1;

Qy	14	HODSEAAINROINLEIYASYVVSYYFDRDVALKHFYFLHQSHEERQHAELMKL	73
Db	4	HQDMINKNEQLNEIYSAANLYLQMSAWC--DDKGFDAAKFLKAHSREEMHQRLLFDY	61
Qy	74	QNQRGGRIFLQDIKKPDCCD 92	
Db	62	LSDTGAMPILGTIEAPPAE 80	

RESULT 11

US-08-818-112-82
Sequence 82, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Devin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedrick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-82

Query Match 10.8%; Score 96.5; DB 3; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

Qy 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHEERQHAELKMLQNORG 78
Db 5 ALMQEQIHNEFTAAQYVAIAVYFDS--LPQLAKHFYSQAVEERNHAMMLVQHLLDRD 62

Qy 79 GRIFLDIKKPCD-----DWESGLNAMECALHLEKNVNSL 115
Db 63 LRVEI-----PGVTVRNQFDRPREALALDQERTVTDQV 98

RESULT 12

US-08-818-111-83
Sequence 83, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818.111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-83

Query Match 10.8%; Score 96.5; DB 3; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

Qy 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHEERQHAELKMLQNORG 78
Db 5 ALMQEQIHNEFTAAQYVAIAVYFDS--LPQLAKHFYSQAVEERNHAMMLVQHLLDRD 62

Qy 79 GRIFLDIKKPCD-----DWESGLNAMECALHLEKNVNSL 115
Db 63 LRVEI-----PGVTVRNQFDRPREALALDQERTVTDQV 98

RESULT 13

US-09-056-556-82
Sequence 82, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056.556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-82

Query Match 10.8%; Score 96.5; DB 3; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

Qy 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSHEERQHAELKMLQNORG 78
Db 5 ALMQEQIHNEFTAAQYVAIAVYFDS--LPQLAKHFYSQAVEERNHAMMLVQHLLDRD 62

Qy 79 GRIFLDIKKPCD-----DWESGLNAMECALHLEKNVNSL 115
Db 63 LRVEI-----PGVTVRNQFDRPREALALDQERTVTDQV 98

RESULT 14

US-09-072-596-83
Sequence 83, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

```

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,967
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.411C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-072-967-82

Query Match 10.8%; Score 96.5; DB 4; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

QY 19 AATNRQINLELYASYVYLSMSYVDFRDDVAKNFAYFLHSHERQHAELKMLQNQRG 78
   | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 ALMQEIHNEFTAAQQYVAIVFYDSED--LPQLAKHFYSQAVEERNHAMMLVQHLDDR 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 79 GRIFLODIKKPDCCD---DWESGLNAMECALHLEKNVNSQL 115
   | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 63 LRVEI-----PGVDYTRNQDFRREALALALDQERTVTDQV 98
   | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: March 30, 2005, 19:42:36
Job time : 23 secs

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